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1/72

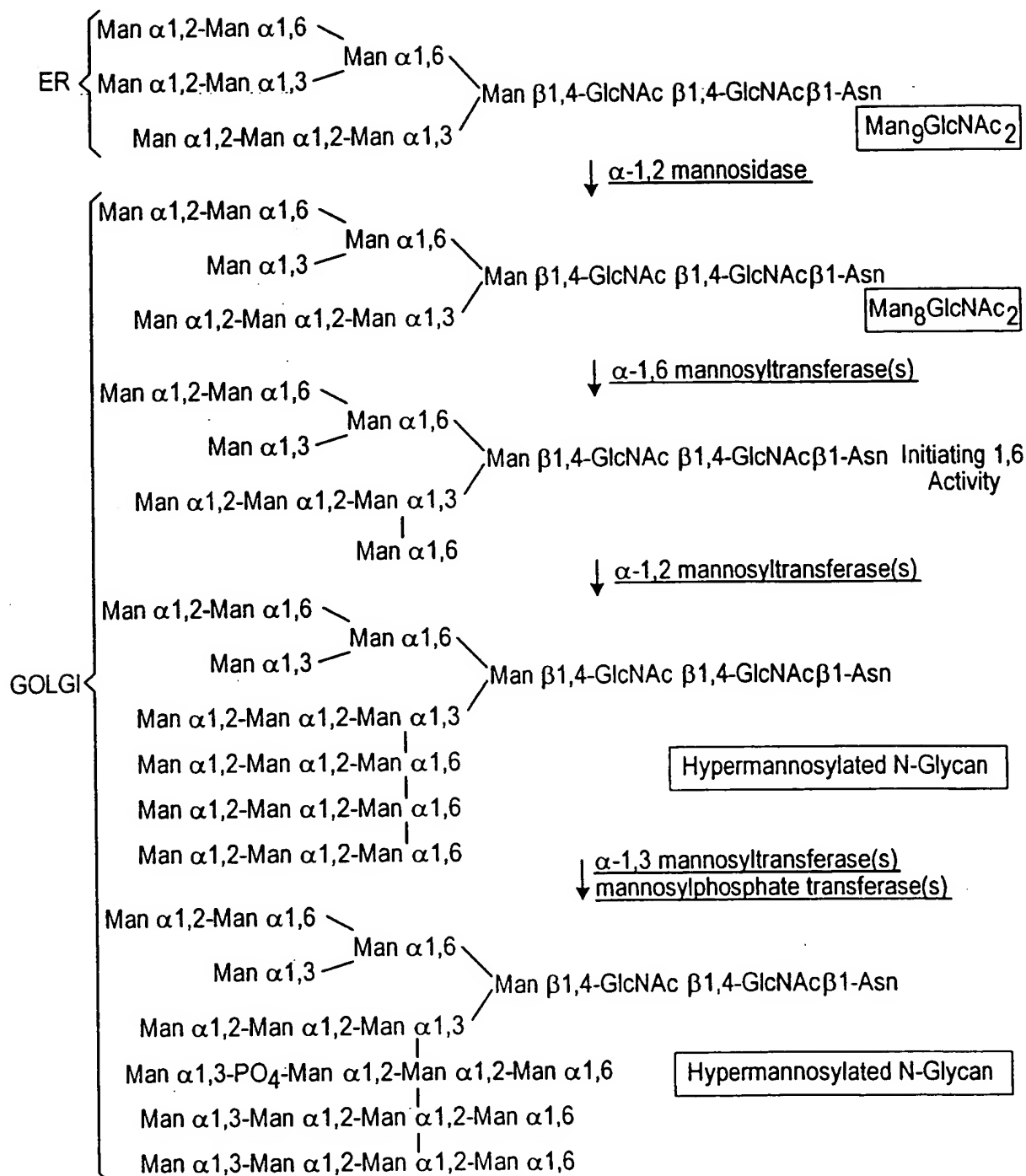


FIG. 1A

2/72

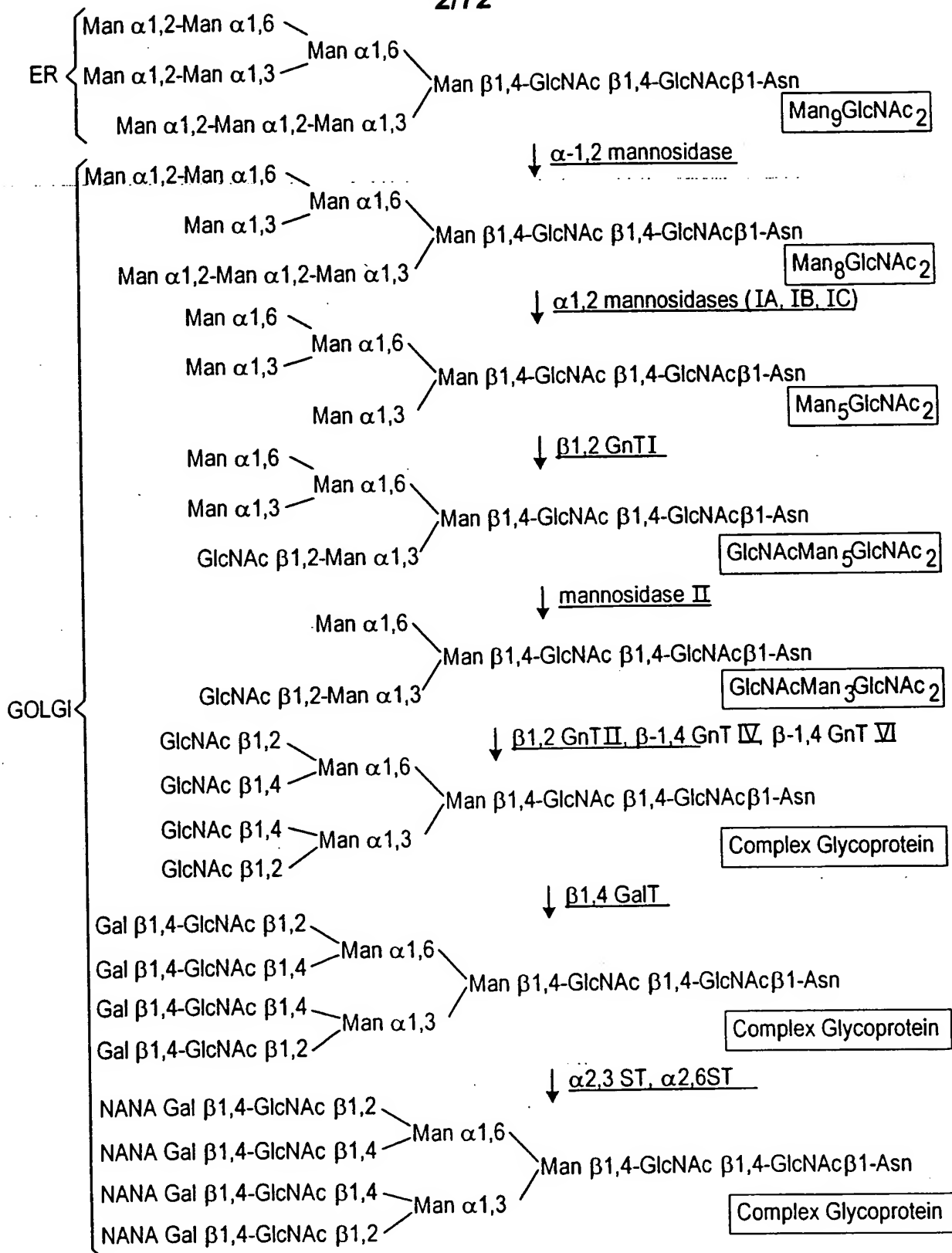


FIG. 1B

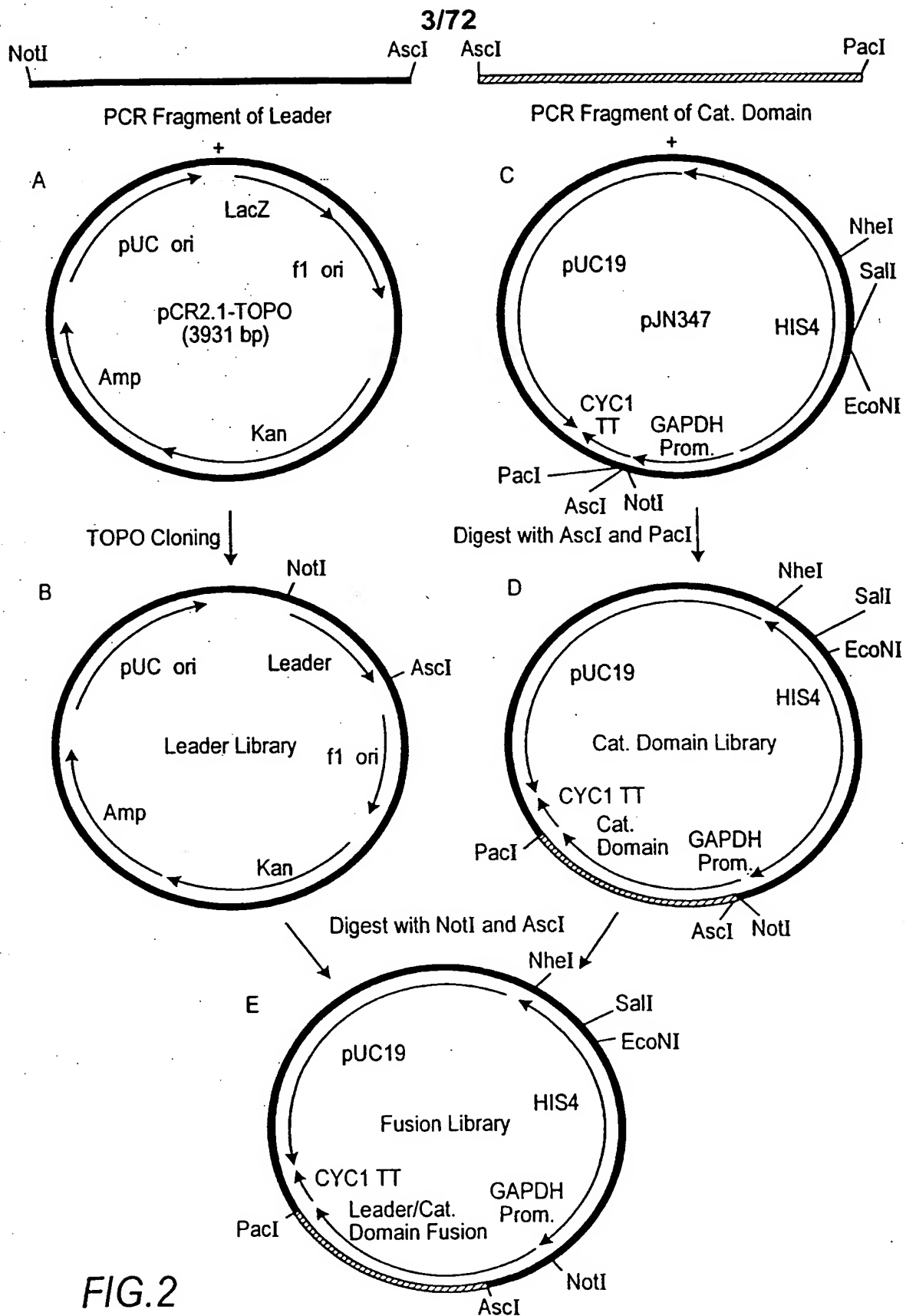


FIG.2

M. musculus alpha-1,2-mannosidase IA open reading frame. The transmembrane and catalytic domains are highlighted in bold respectively. The sequence of the primers used to generate the N-terminal truncations are highlighted by underlining and the start of each respective protein fragment indicated by an arrow.

```

1  atgccgtggggcctgttgccgctcttcagtagccctggggcgggcgccctgggcagtgccctgggggggcttgccggcgaggagggg
1▶ M P V G G L L P L F S S P G G G L G S G L G G L G G L G G R K G
97  tctggcccgctgccttcgcctcaccgagaagtctgtgtgtgttcagcgcccttcacgcgtotgttcgggggcaatc
33▶ S G P A A F R L T E K F V L L V F S A F I T L C F G A I
184  ttcttctgctgactcctccaaagtctcagcgggtcctgttcactccaaacctgttcagcccgccggcgagcacaagcccggtctcg
62▶ F F L P D S S K L L S G V L F H S N P A L Q P P A E H K P G L
      d65 primer
278  gggcgctgcgaggatgcccgccgaggaggagagtcgcgcaccgcgaggaaagcgcgccctggggaccctggagctggactggaagacaacttagcca
93▶ G A R A E D A A E G R V R H R E E G A P G D P G A G L E D N L A
      d105 primer
374  ggatccgcgaaaccacgagcgggctctcagggaagccaaaggagaccctgcagaagctgccggaggagatcccaagagacattctgctggagaagg
125▶ R I R E N H E R A L R E A K E T L Q K L P E I Q R D I L L E K
470  aaaaggtggccaggaccagctgcgtgacaaggatctgtttaggggcttgcccaaggtggacttccctgcccccggtcggttagagaacgggagc
157▶ E K V A Q D Q L R D K D L F R G L P K V D F L P P V G V E N R E
      d187 primer
566  ccgtgacgccaccatccgtgagaagaggggcaagatcaaaagagatgatgaccccatgcttggaataattataacgctatgcgtggggc
189▶ P A D A T I R E K R A K I K E M M T H A W N N Y K R Y A W G

```

FIG. 3

655 ttgaacgaactgaaacctatatcaaaagaaggccattcaagcagttgtttggcaacatcaaaaggagctacaatagtagatg
219▶ L N E L K P I S K E G H S S S L F G N I K G A T I V D
737 cctggatacccttttcattatgggcatgaagactgaatttcaagaagctaaatcgtgattaaaaataatttagatttttaa
246▶ A L D T L F I M G M K T E F Q E A K S W I K K Y L D F N
819 tgtgaatgctgaagtttctgttttgaagtcaacatacgtctcgtcgttggaactgctgcagcctactattgtccggagag
273▶ V N A E V S V F E V N I R F V G G L L S A Y Y L S G E
901 gatatattcgaaagaagcagtggaacttggggttaaattgctacctgcatttcatactccctctggaataccttgggcgat
301▶ E I F R K K A V E L G V K L L P A F H T P S G I P W A
983 tgotgaatatgaaaagtgggagtcggggaactggccctggccctctggaggcagcagtagtacctgcccgaatttggaaactct
328▶ L L N M K S G I G R N W P W A S G G S S I L A E F G T L
065 gcatttagagtttatgcacttgtccacttatcaggagaccagctctttgccgaaaaggttatgaaaattcgaacagtggtg
355▶ H L E F M H L S H L S G D P V F A E K V M K I R T V L
1147 acaaaactggacaaaccagaaggccctttatcctaactatctgaacccagtagtggacagtggggtccaacatcatgtgtcgg
383▶ N K L D K P E G L Y P N Y L N P S S G Q W G Q H H V S
2229 ttggaggacttgagacagcttttatgaatatatttgcctaaaggctgggttaattgtctgacaagacagatctcgaagccaaaga
410▶ V G G L G D S F Y E Y L L K A W L M S D K T D L E A K K
311 gatgtatttgatgctgttcaggccatcgagactcaacttgatccgcgaagtcaagtgggggaactaacgtacatcgcagagtgg
437▶ M Y F D A V Q A I E T H L I R K S S G G L T Y I A E W
393 aagggggccctcctggaacacaagatgggccacctgacgtgctttgcaggaggcagctgtttgcacttgggcagatggagctc
465▶ K G G L L E H K M G H L T C F A G G M F A L G A D G A
1475 cggaagcccgggcccaacactaccttgaactcgagctggaattggccgcacttgcattgaatcttataatcgtagcatatgt
492▶ P E A R A Q H Y L E L G A E I A R T C H E S Y N R T Y V
1557 gaagttgggacggagcgtttcgaatttgatggcgtgtggaagctattgccacgagcgcaaaatgaaaagtatttaoatctta
519▶ K L G P E A F R F D G G V E A I A T R Q N E K Y Y I L
1639 cgccccgggtcatcgagacatacatgtacatgtggcgaactgactcaagaccccaagtagcaggacctgggcctgggaagccg
547▶ R P E V I E T Y M Y M W R L T H D P K Y R T W A W E A
1721 tggaggtctagaagtcactgcagagtgaaoggaggtactcaggcttacgggatgtttacattgcccgtgagagttatga
574▶ V E A L E S H C R V N G G Y S G L R D V Y I A R E S Y D
1803 cgatgtccagcaagtttctcctggcagagacactgaagtatttgtactgtatattttccgatgatgaccttcttccacta
601▶ D V Q Q S F F L A E T L K Y L Y L I F S D D L L P L
1895 gaacactggatcttcaaacacgaggctcatccttccctatactccgtgaacagaagagaaattgatggcaagagaatga
629▶ E H W I F N T E A H P F P I L R E Q K E I D G K E K

FIG. 3 CONT

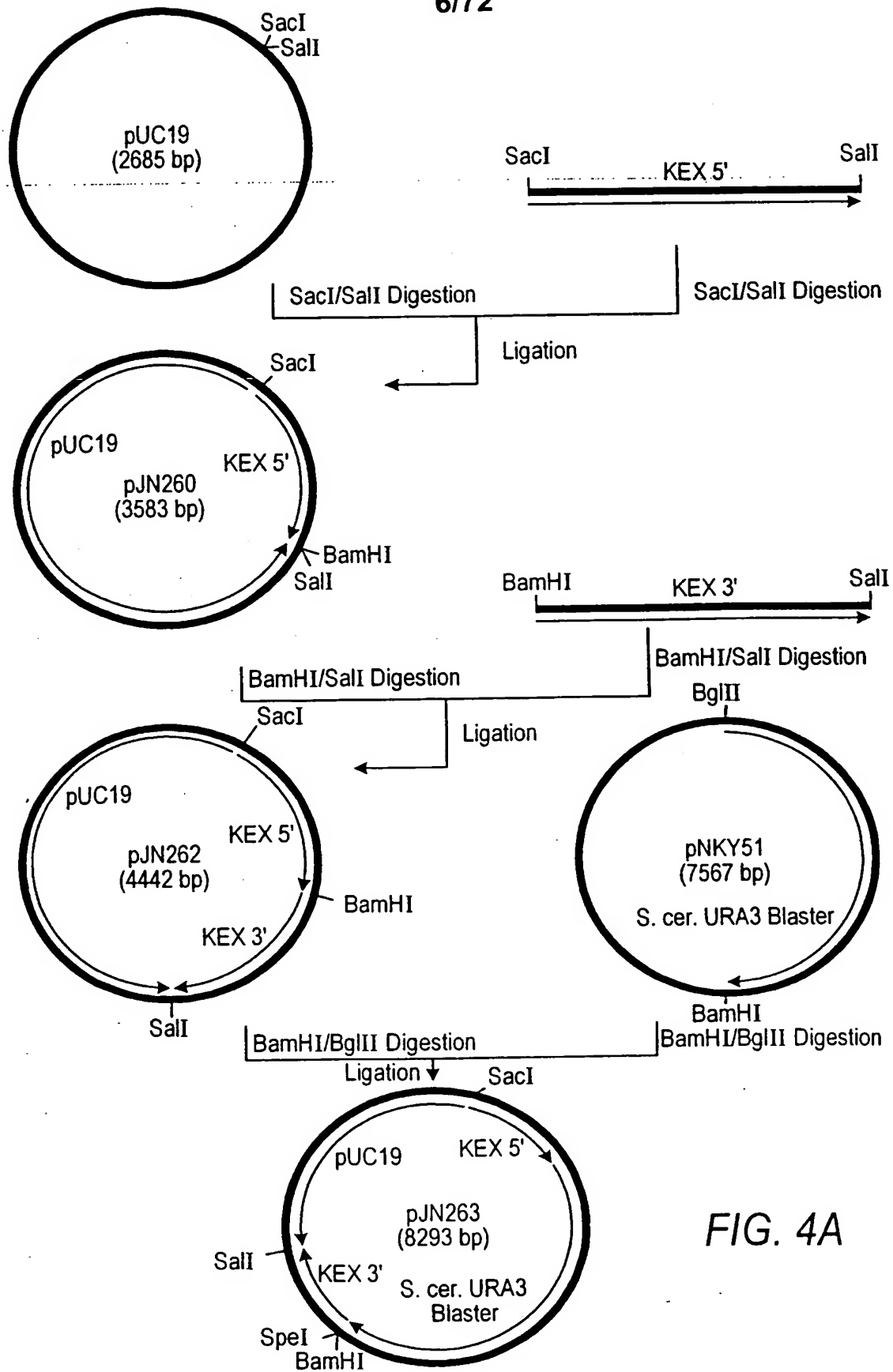


FIG. 4A

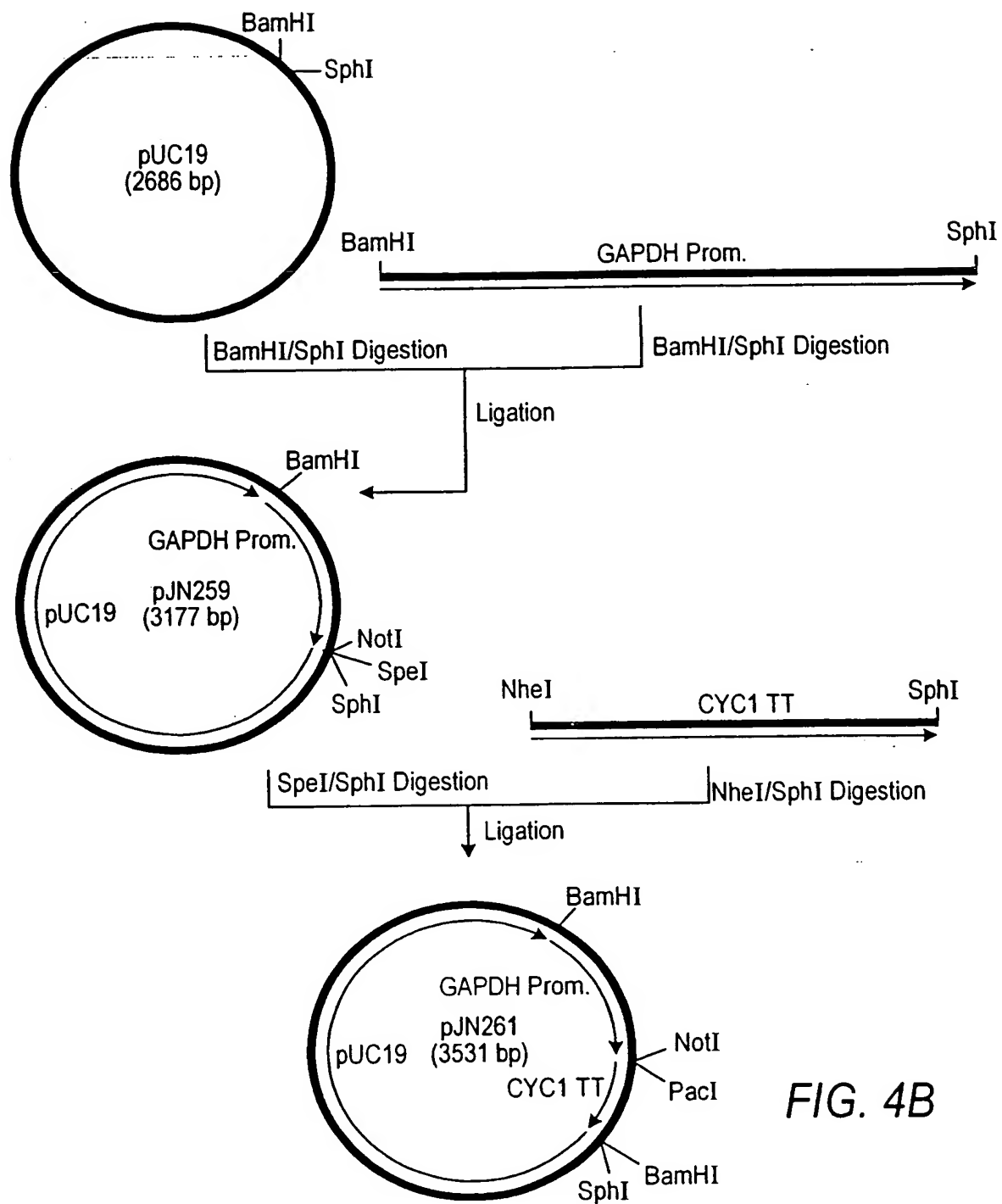


FIG. 4B

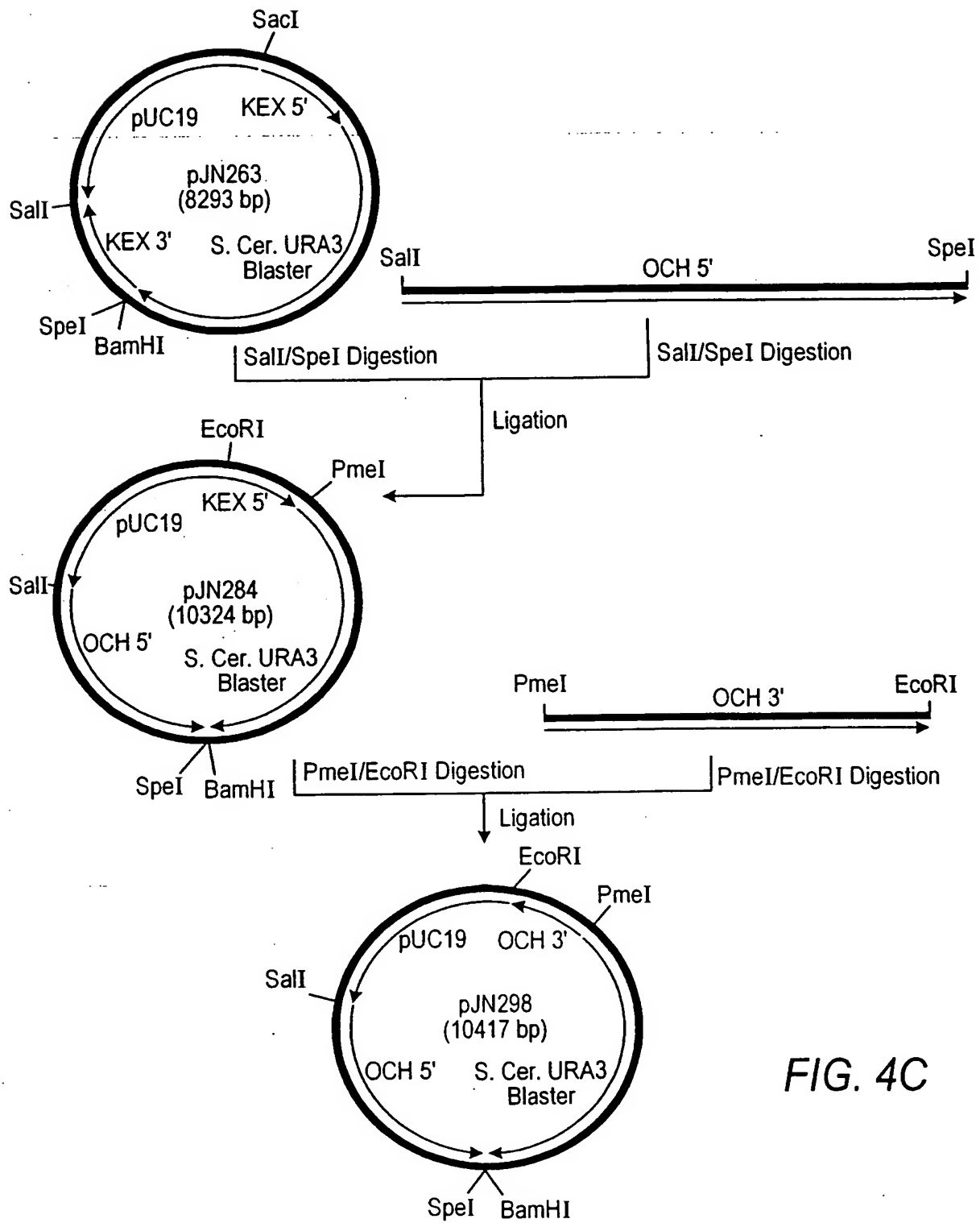


FIG. 4C

9/72

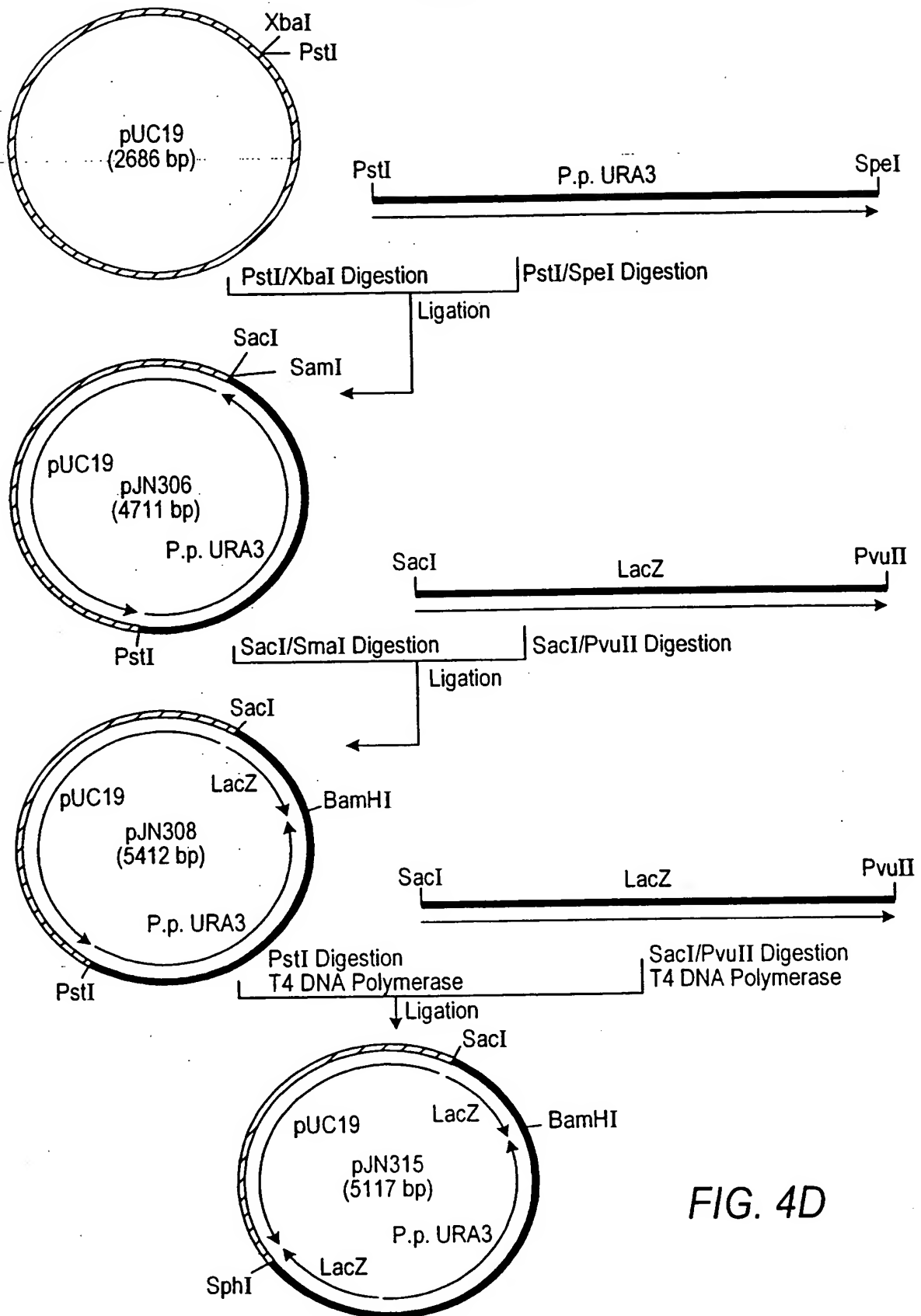


FIG. 4D

10/72

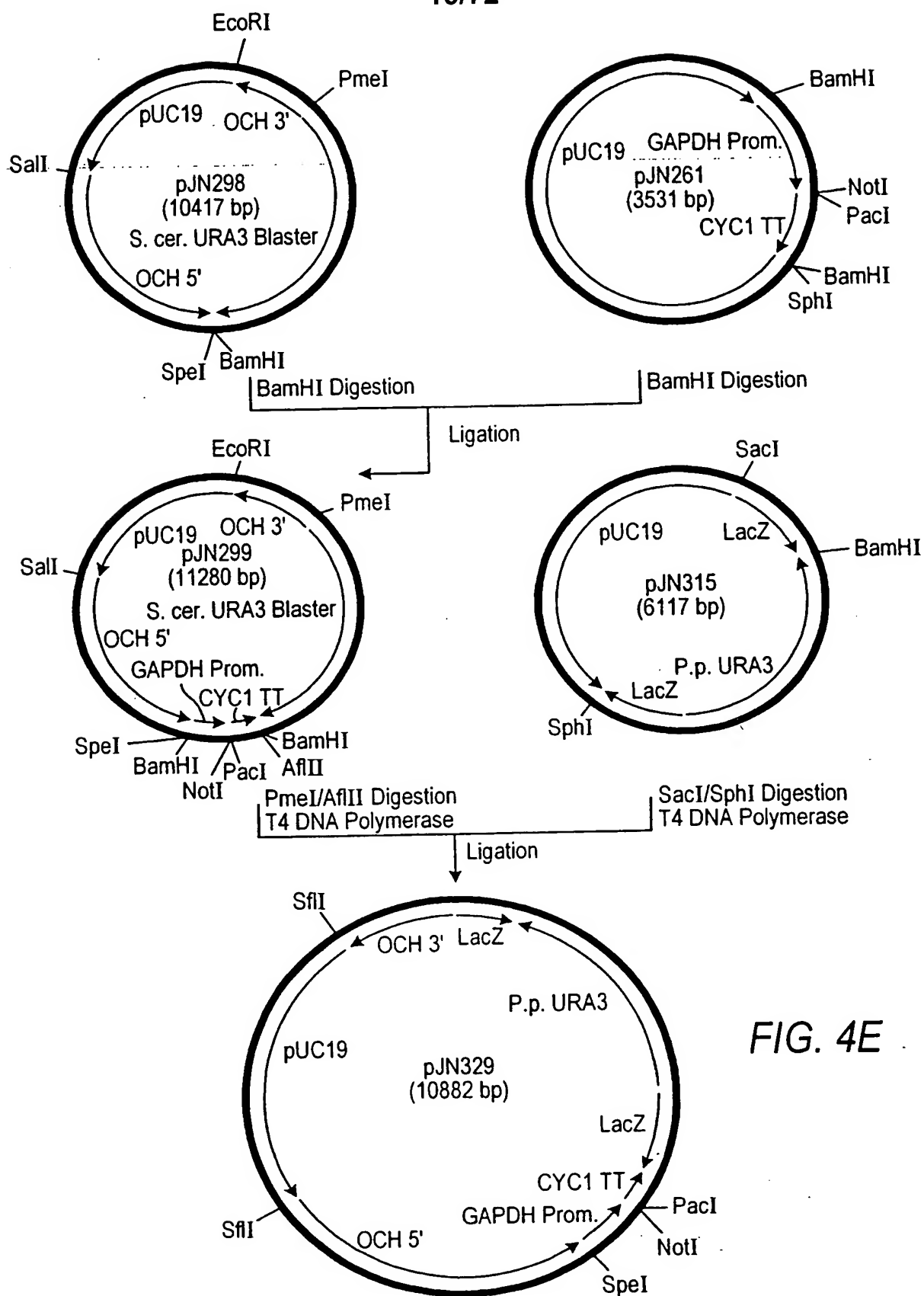


FIG. 4E

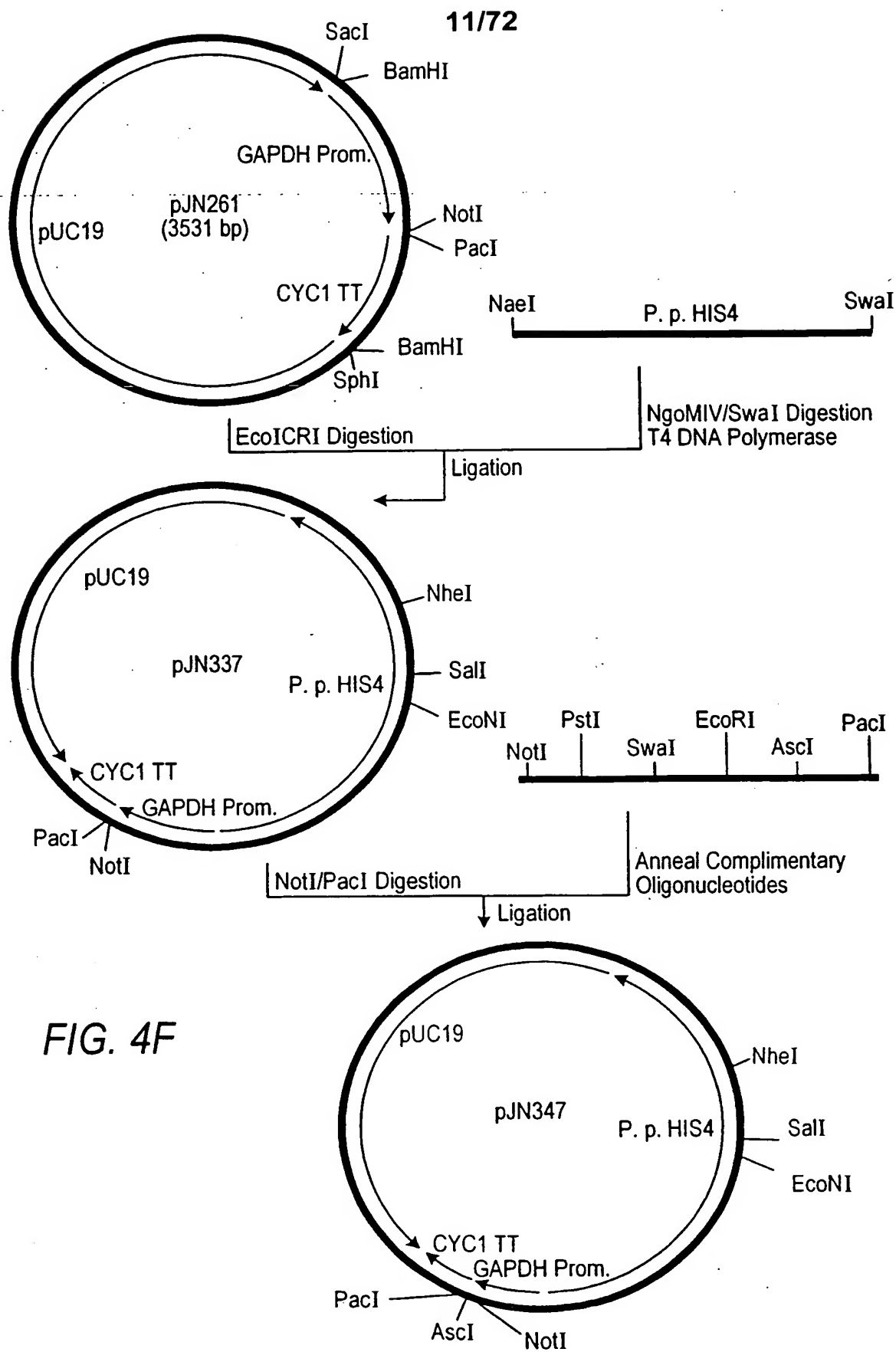
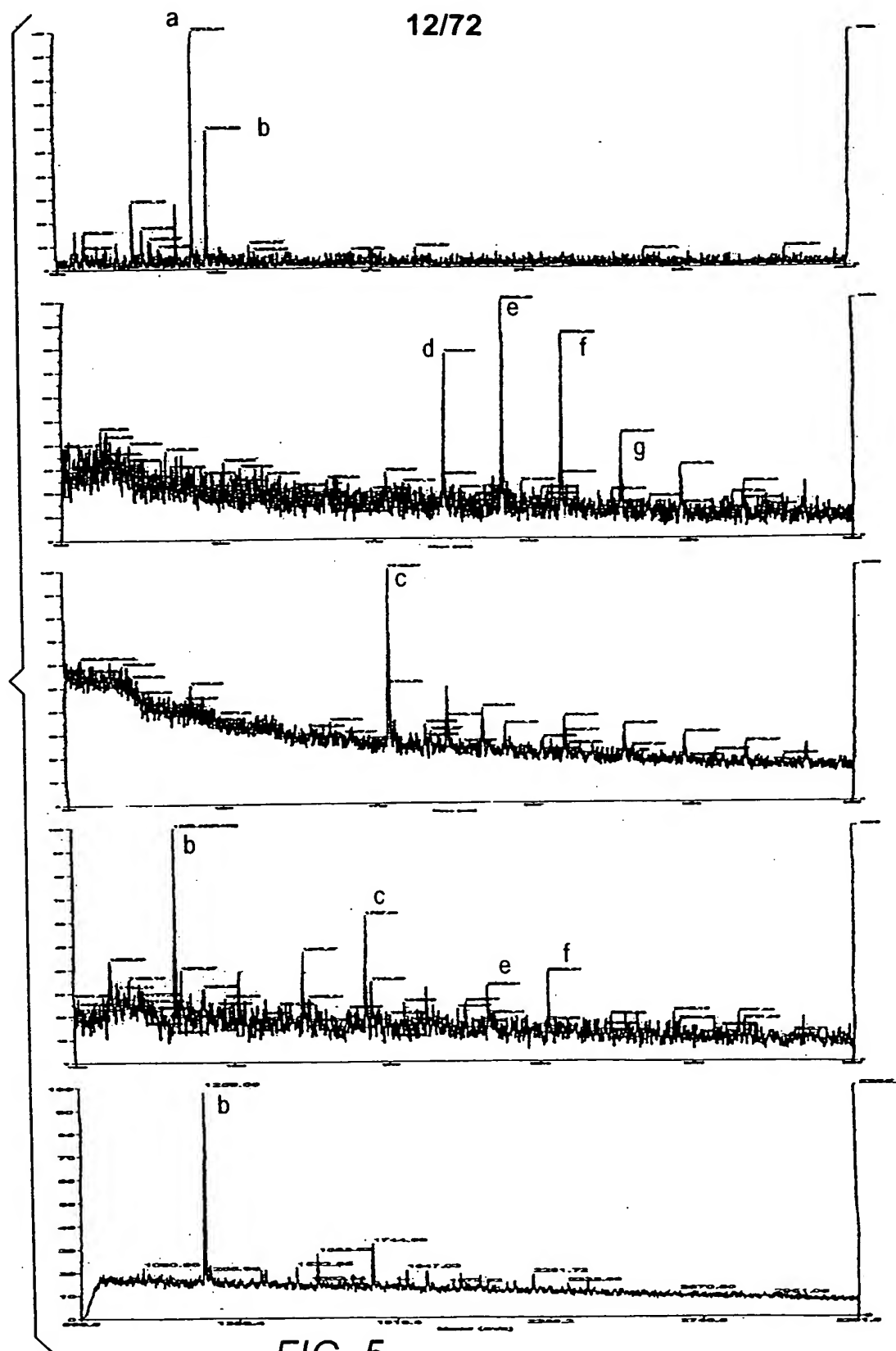


FIG. 4F



13/72

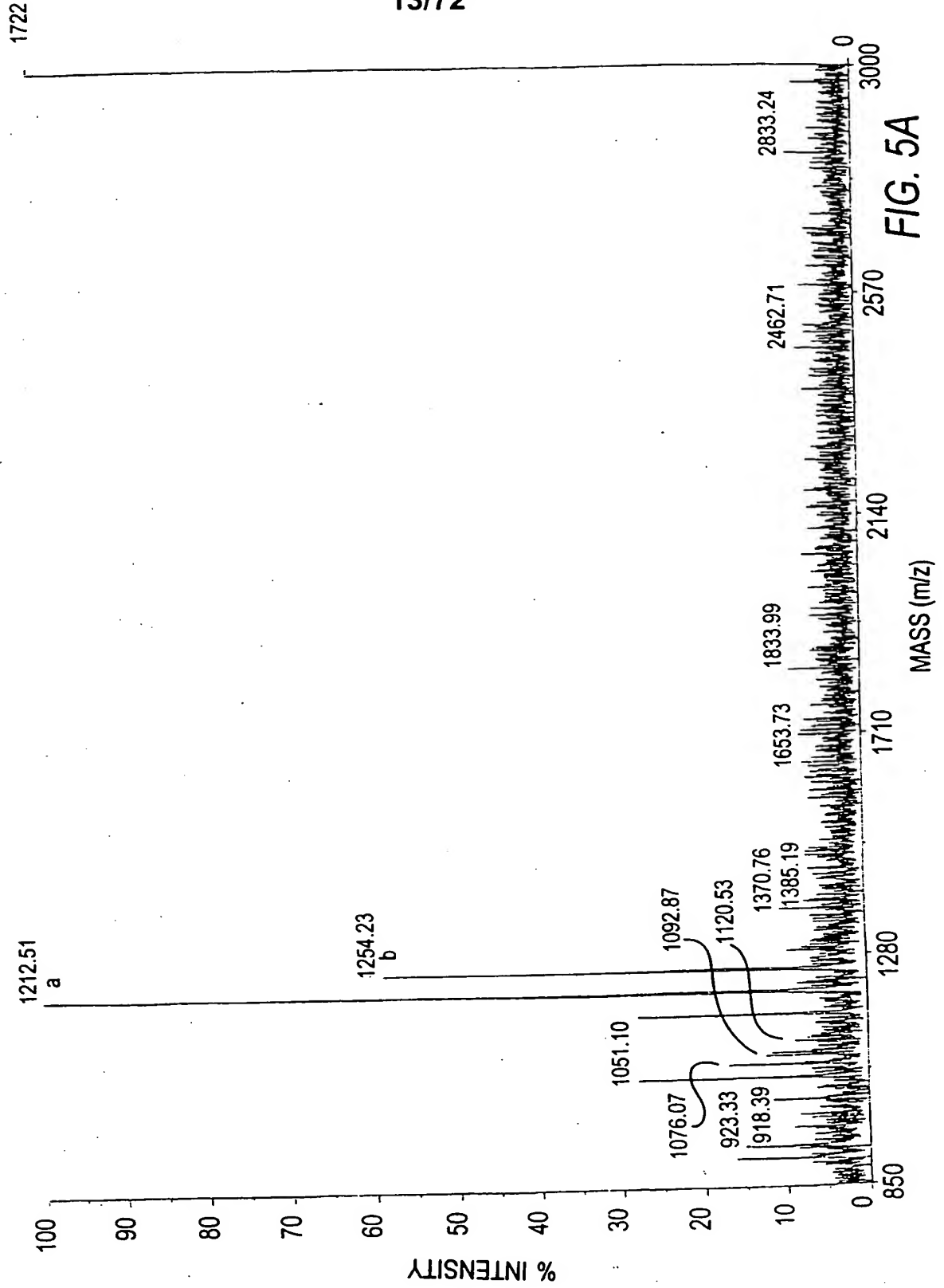


FIG. 5A

14/72

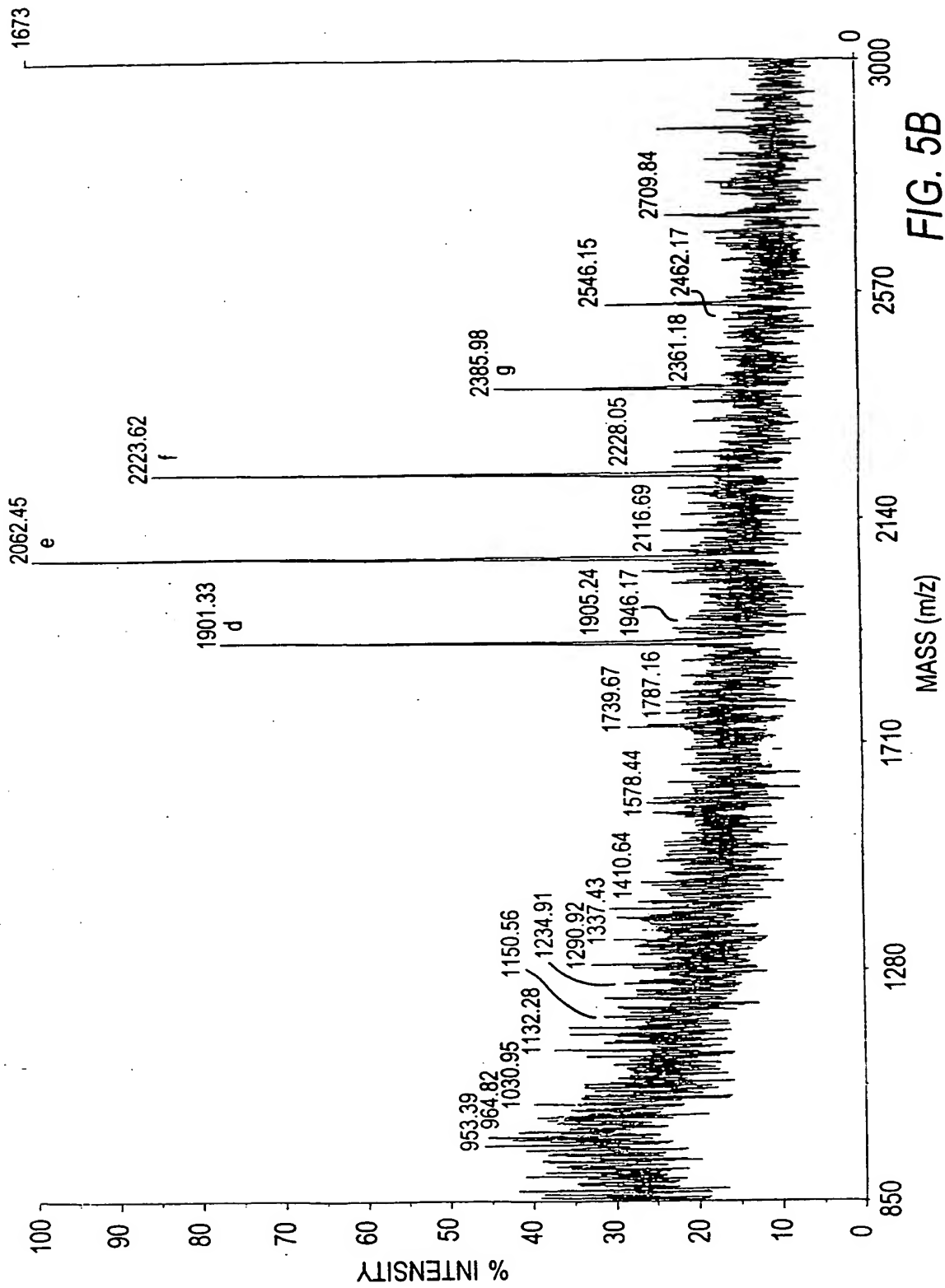


FIG. 5B

15/72

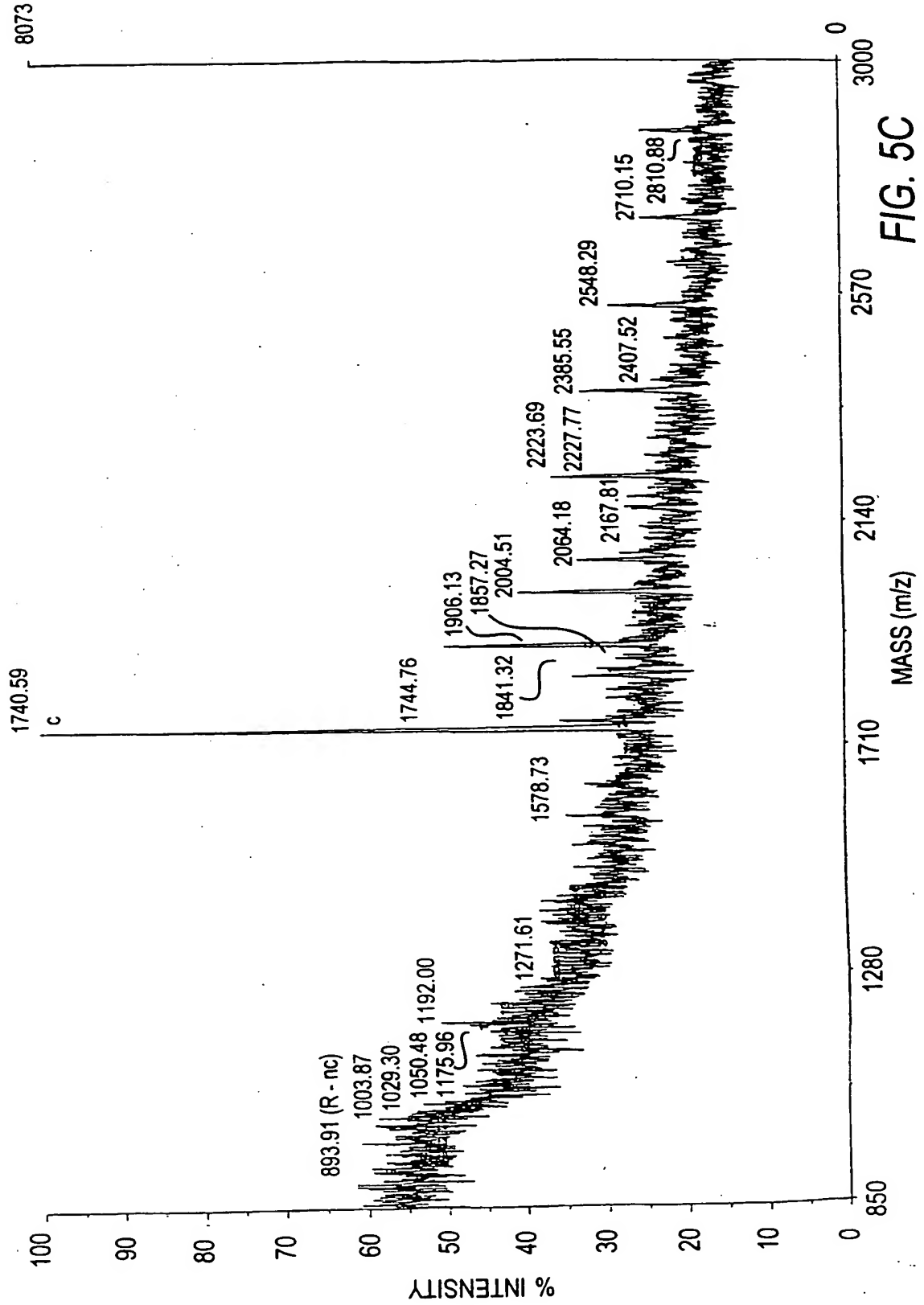


FIG. 5C

16/72

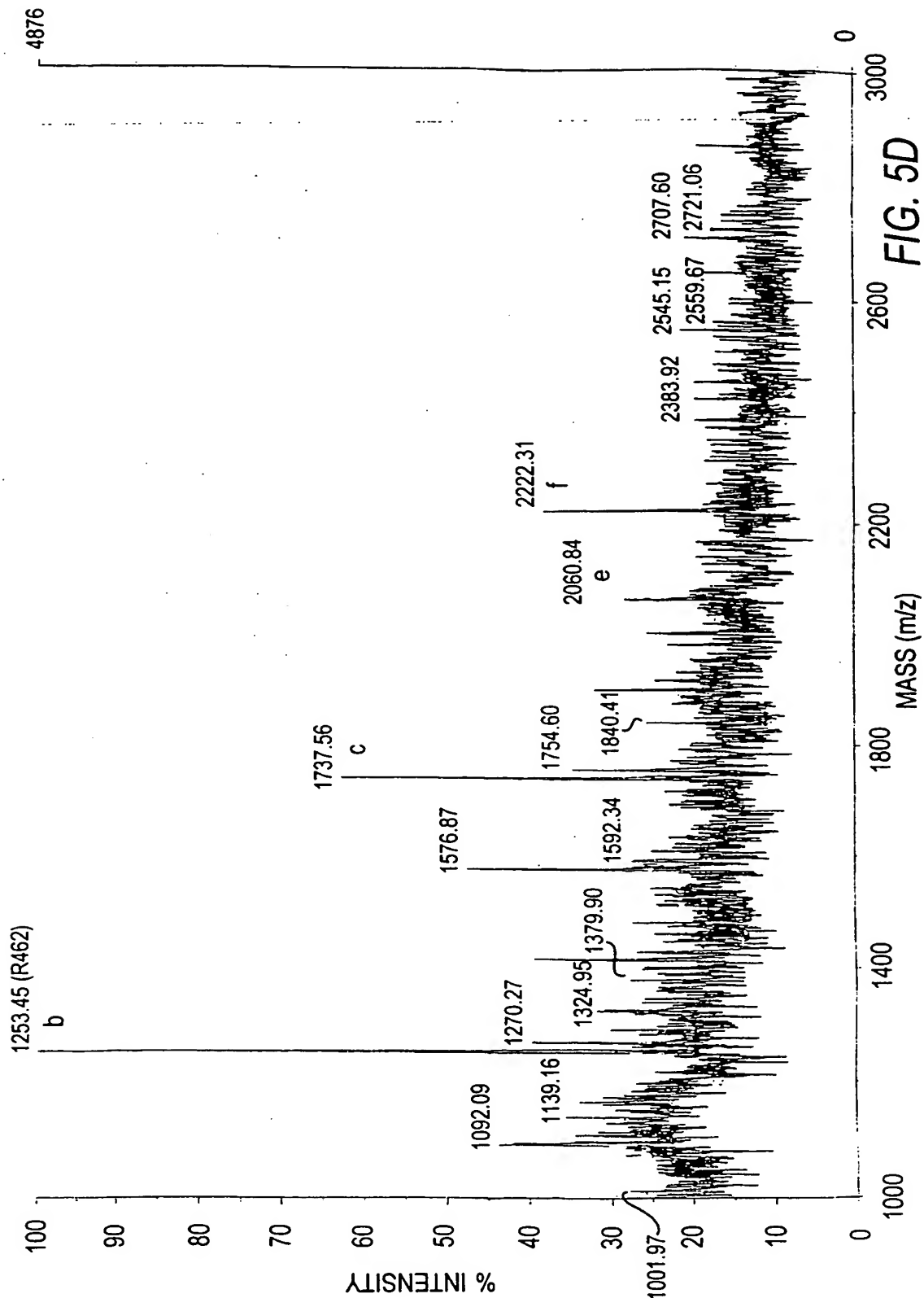


FIG. 5D

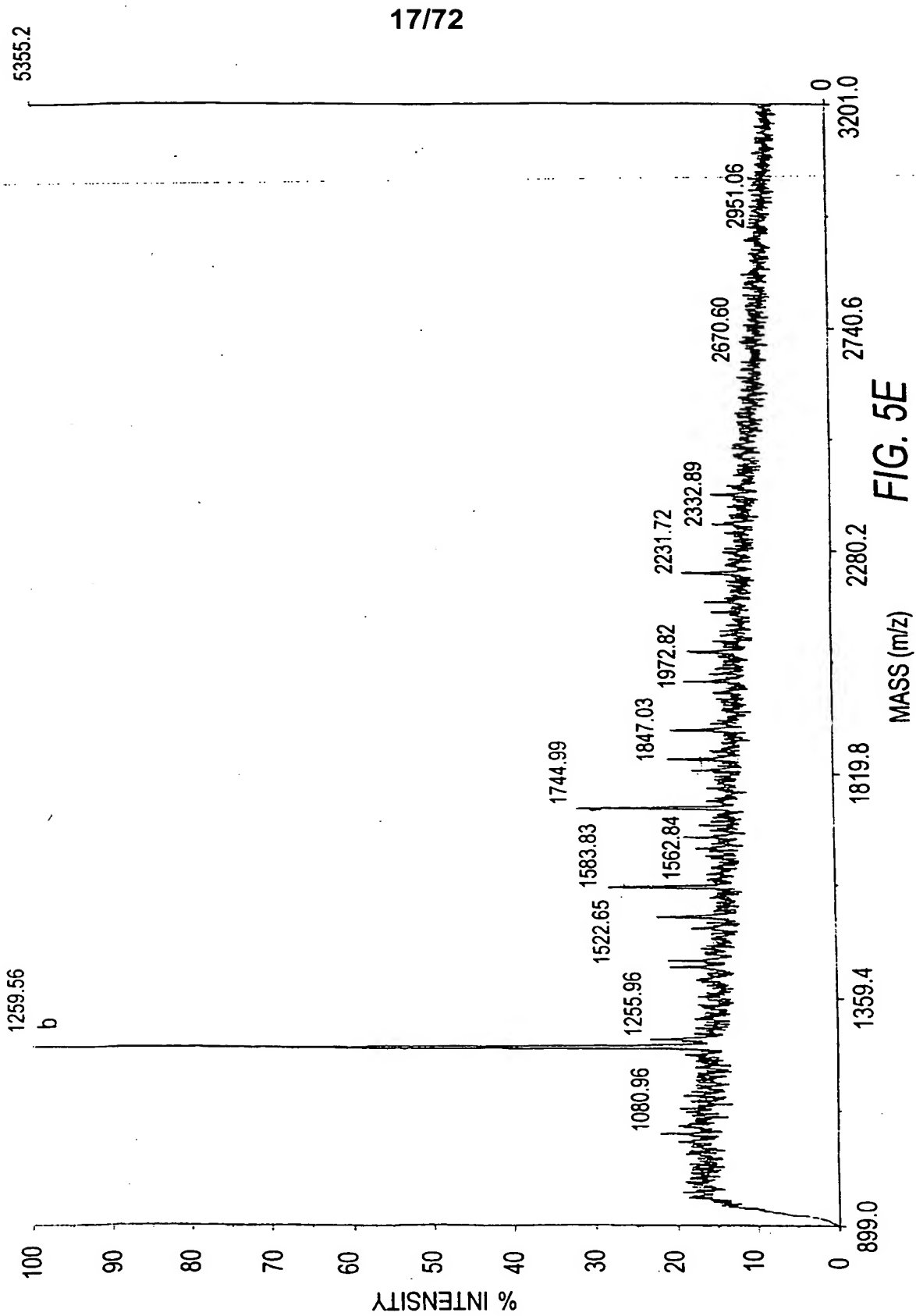


FIG. 5E

18/72

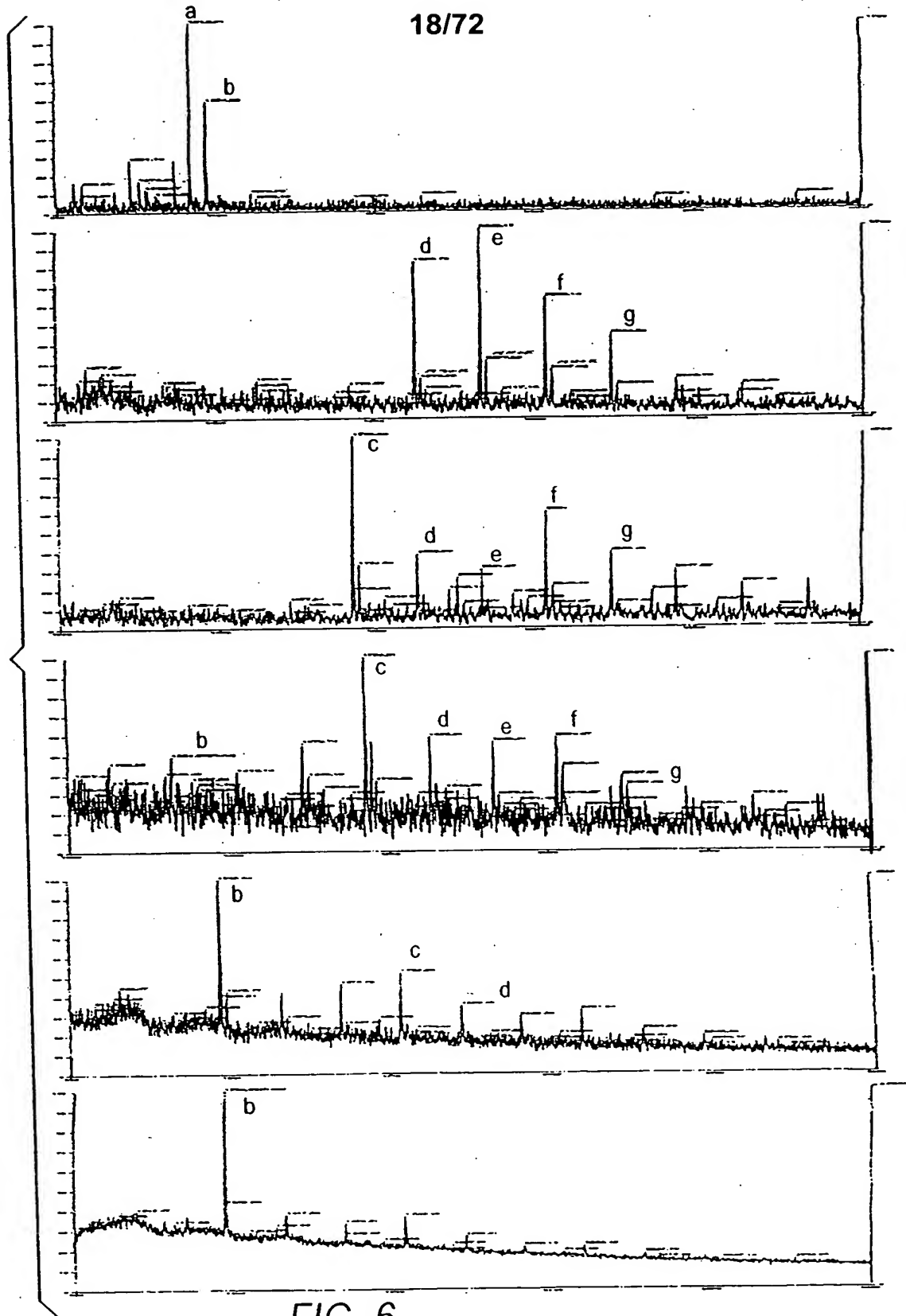
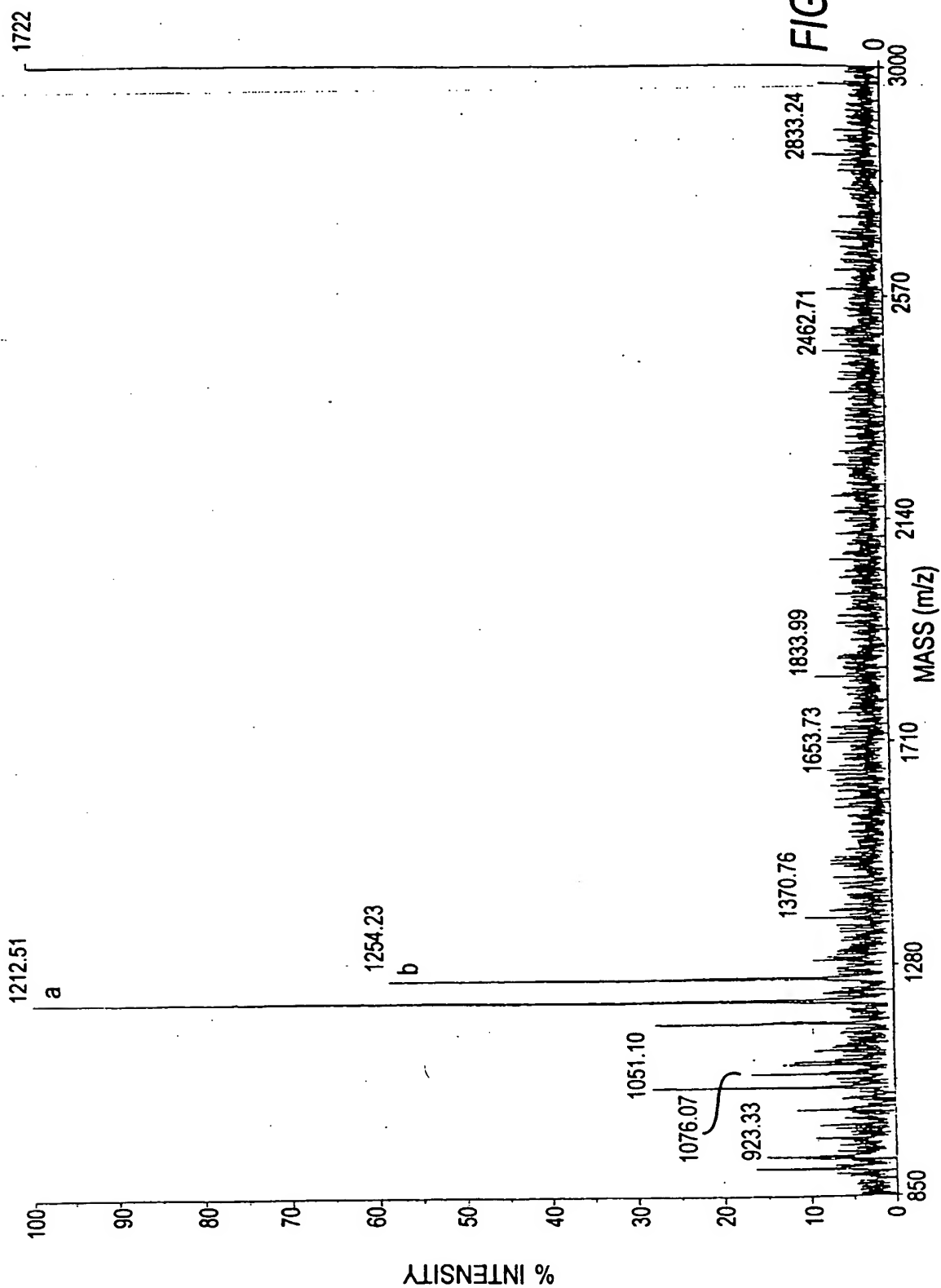


FIG. 6

19/72



20/72

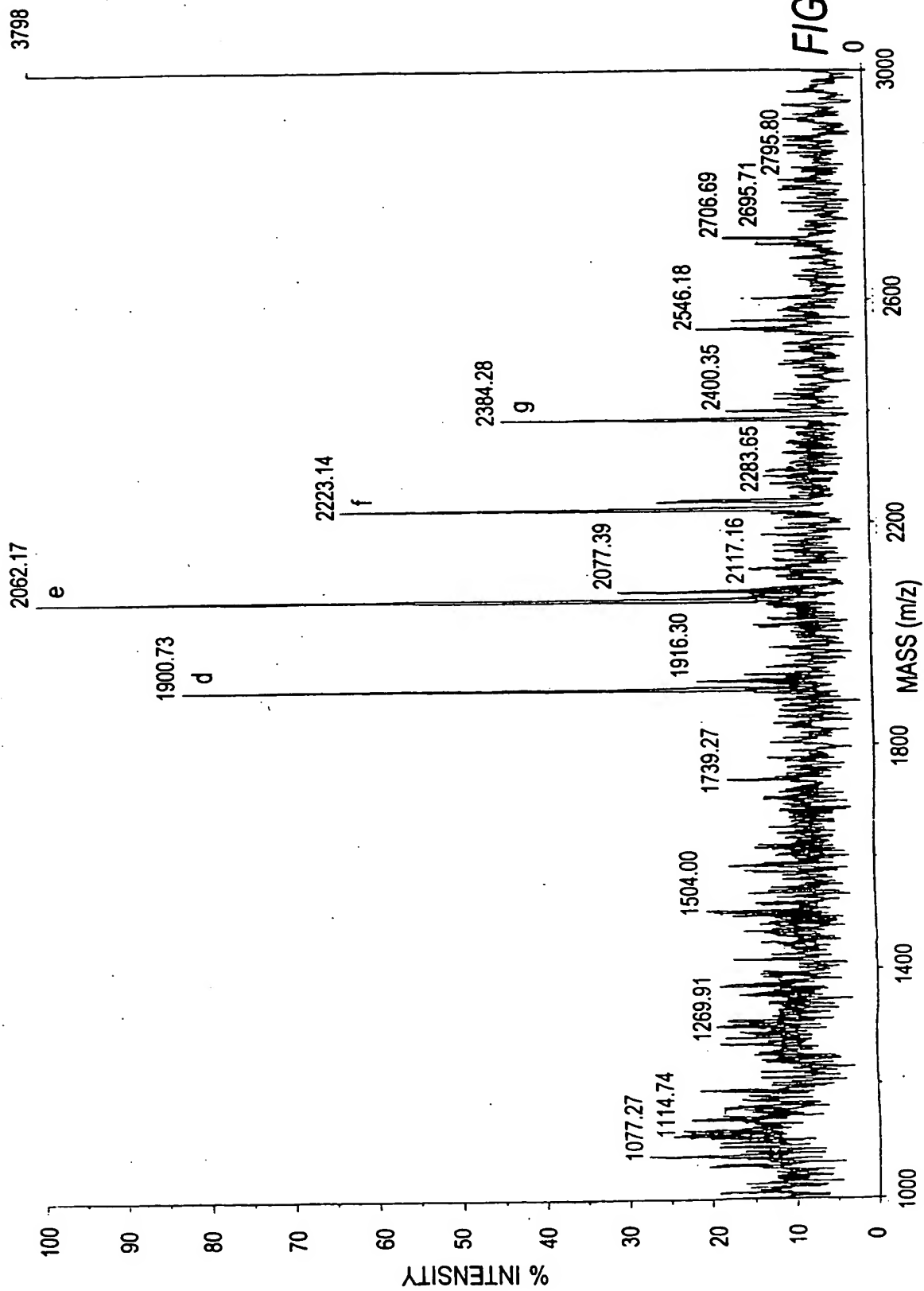


FIG. 6B

21/72

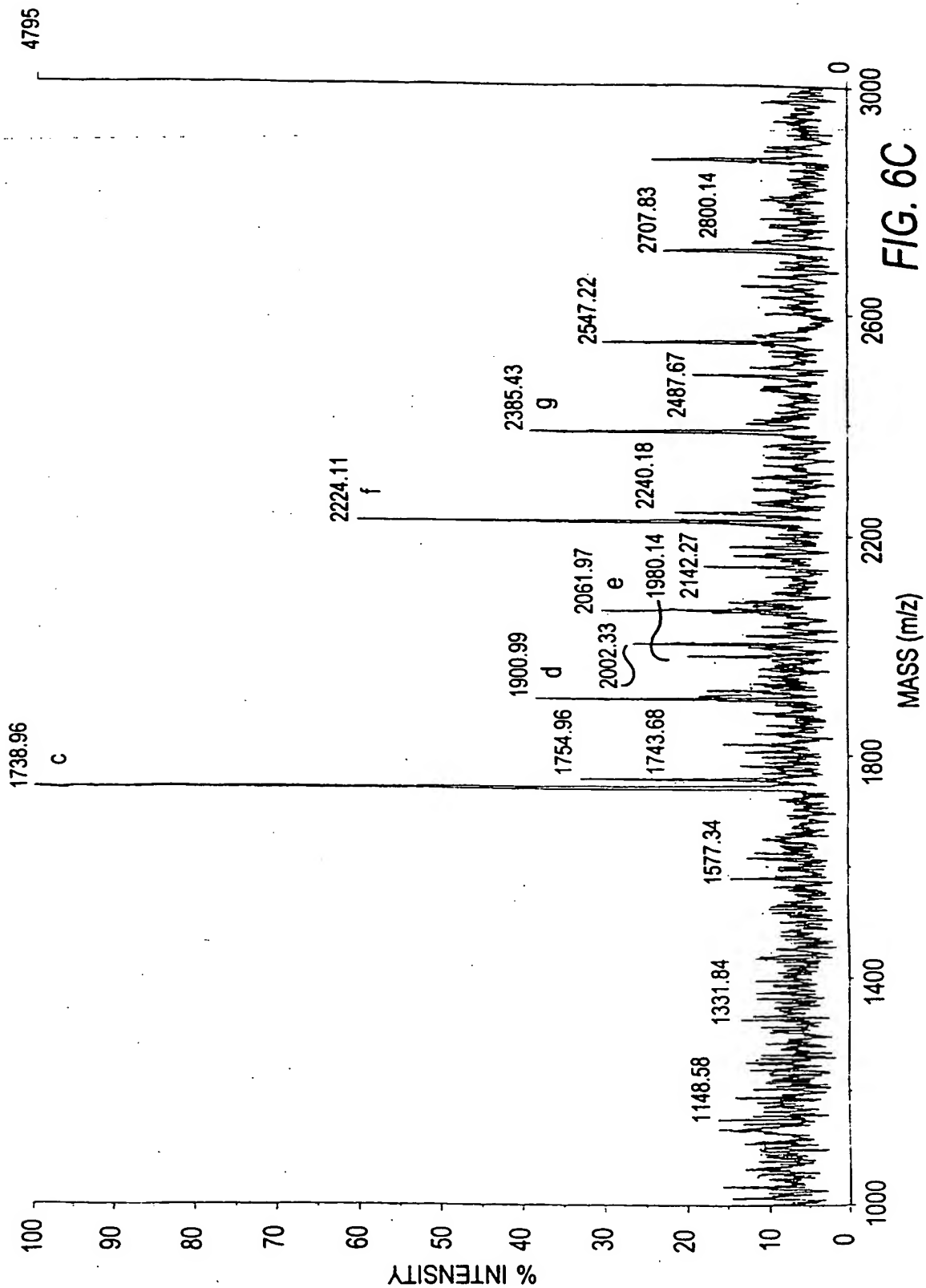


FIG. 6C

22/72

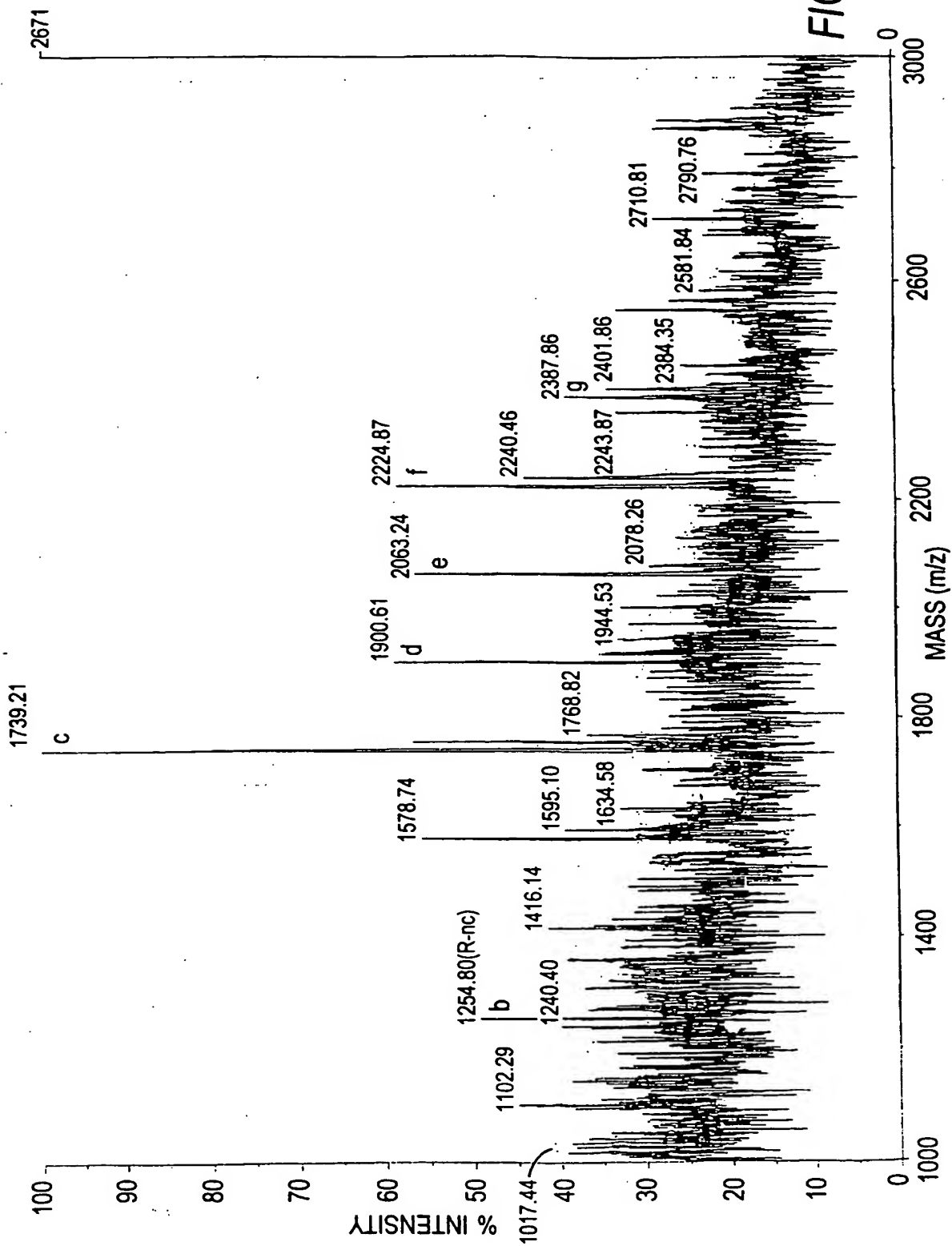


FIG. 6D

23/72

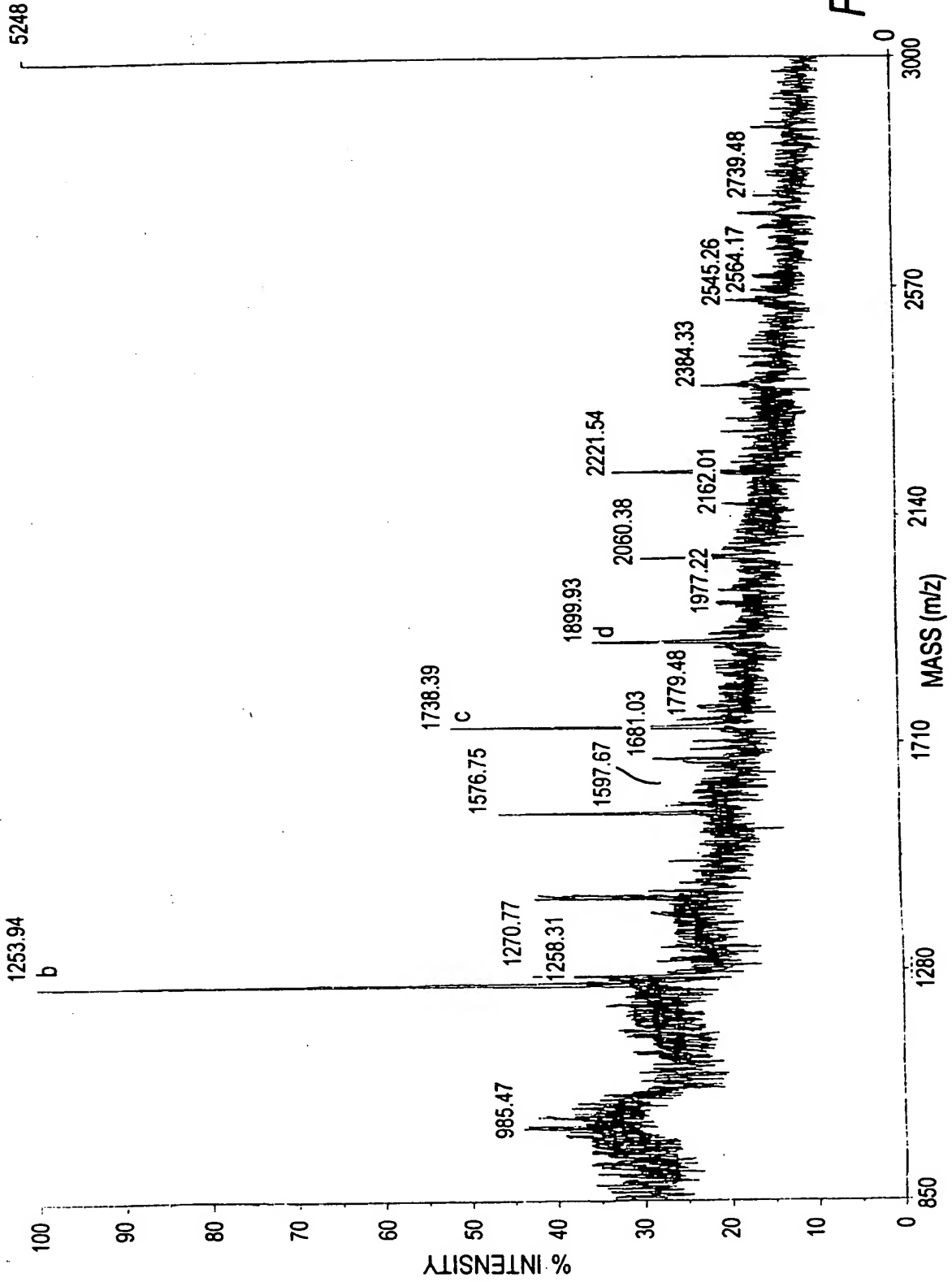


FIG. 6E

24/72

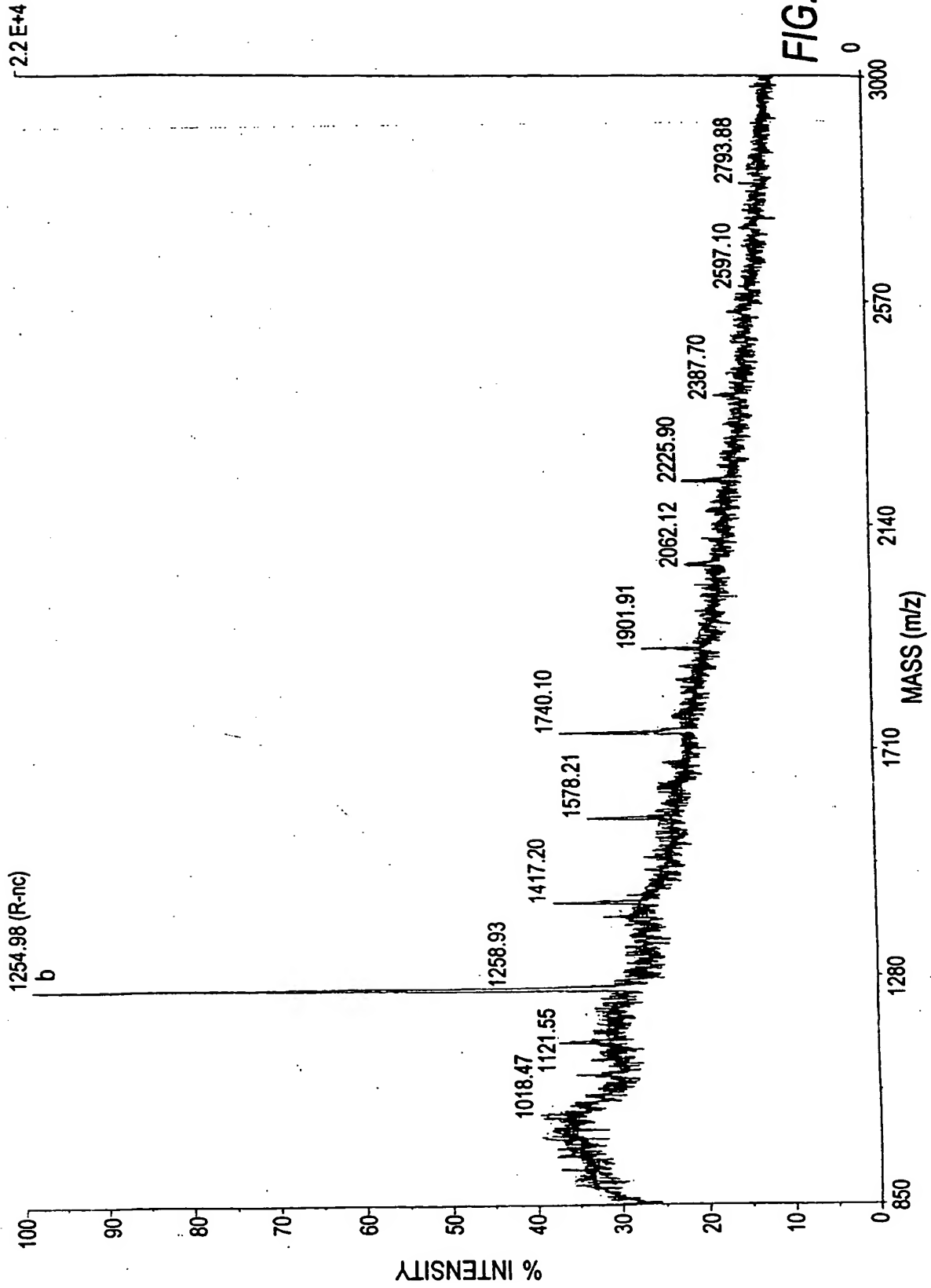


FIG. 6F

25/72

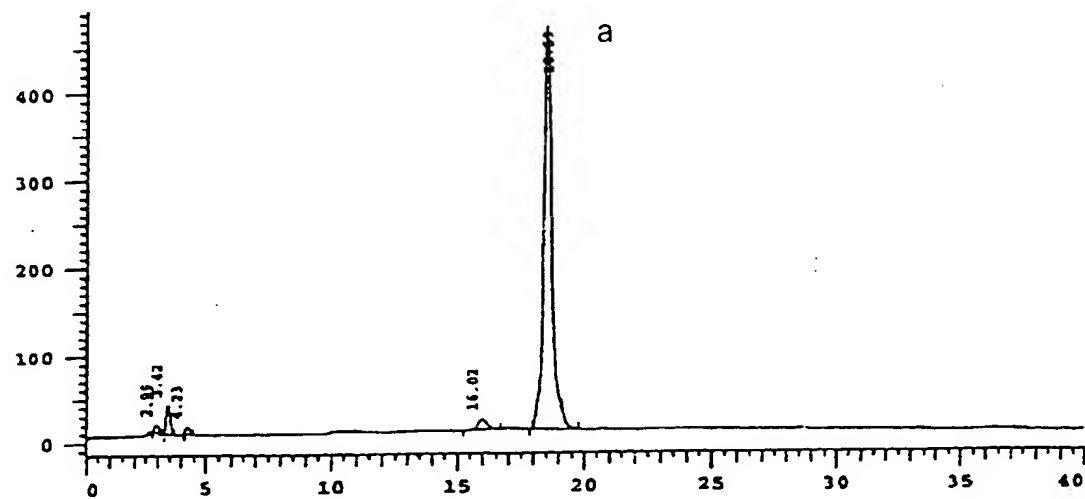
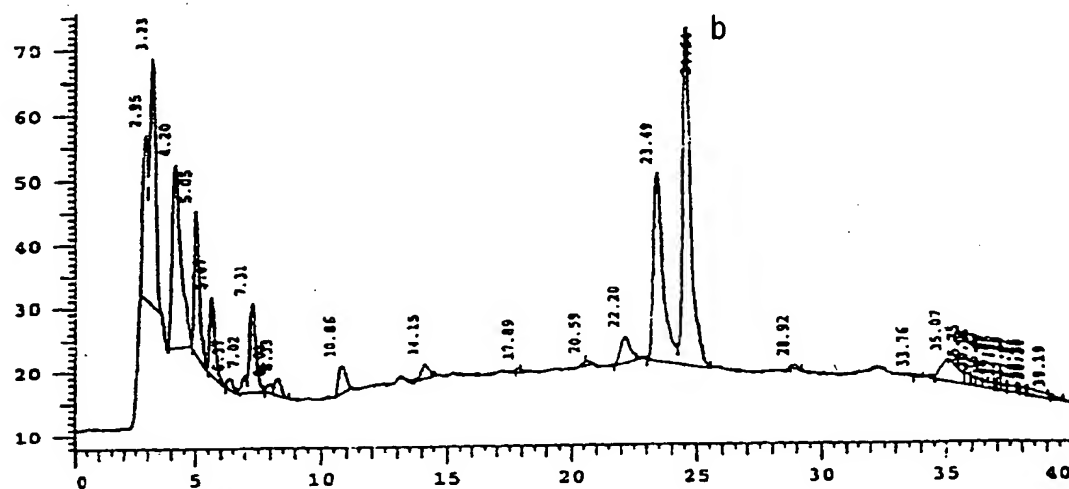
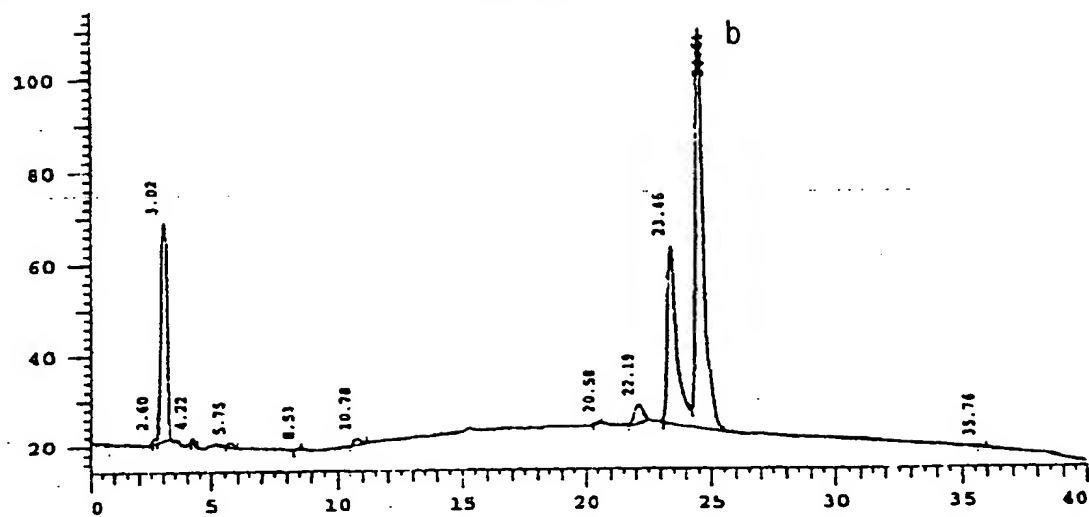


FIG. 7

26/72

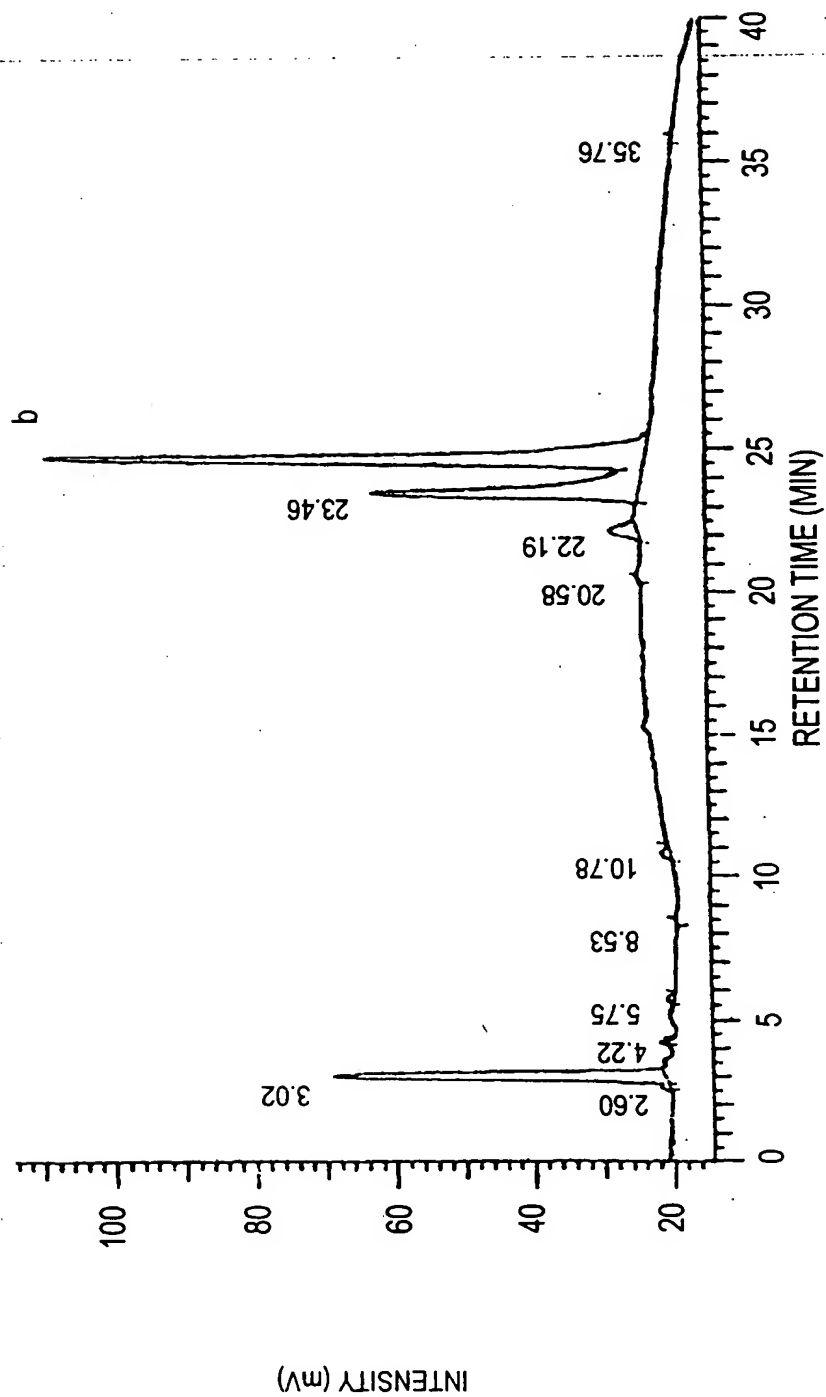


FIG. 7A

27/72

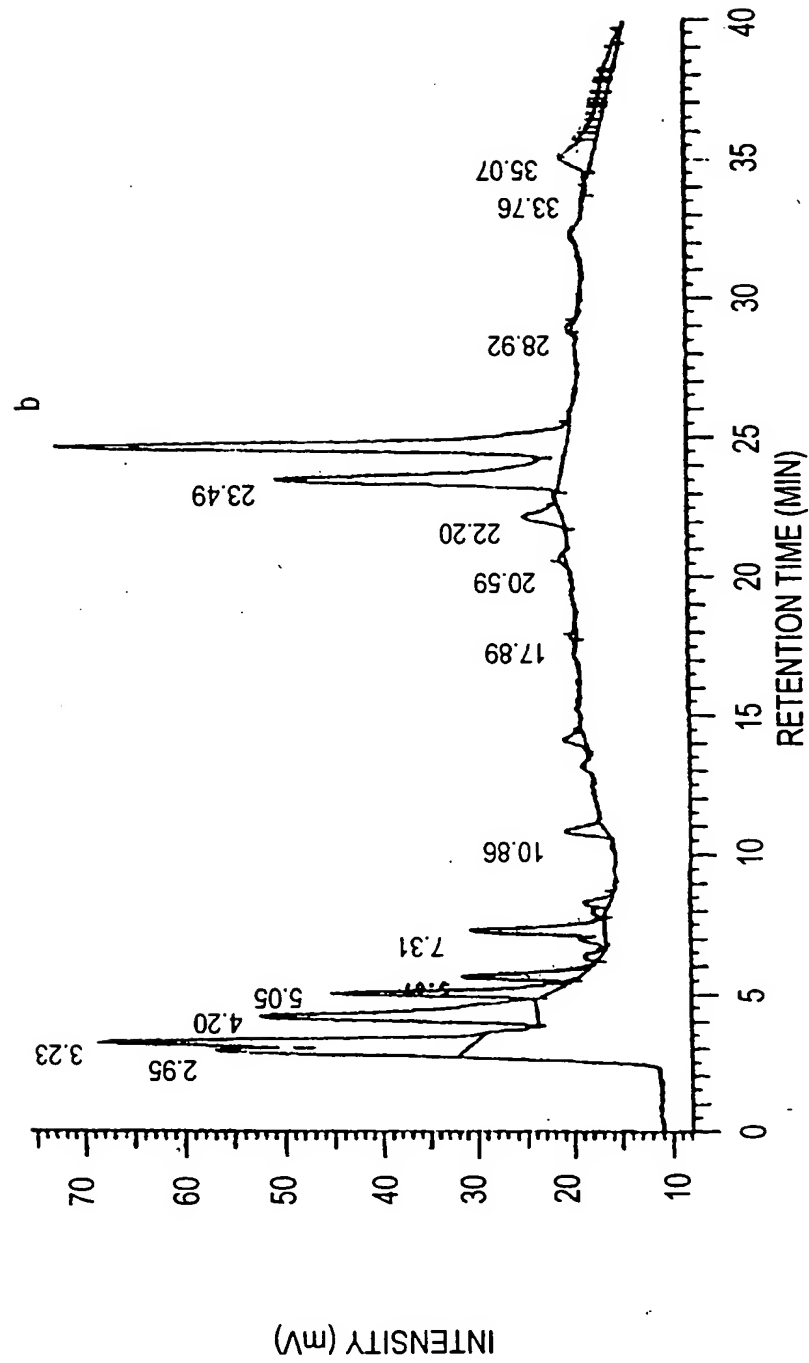


FIG. 7B

28/72

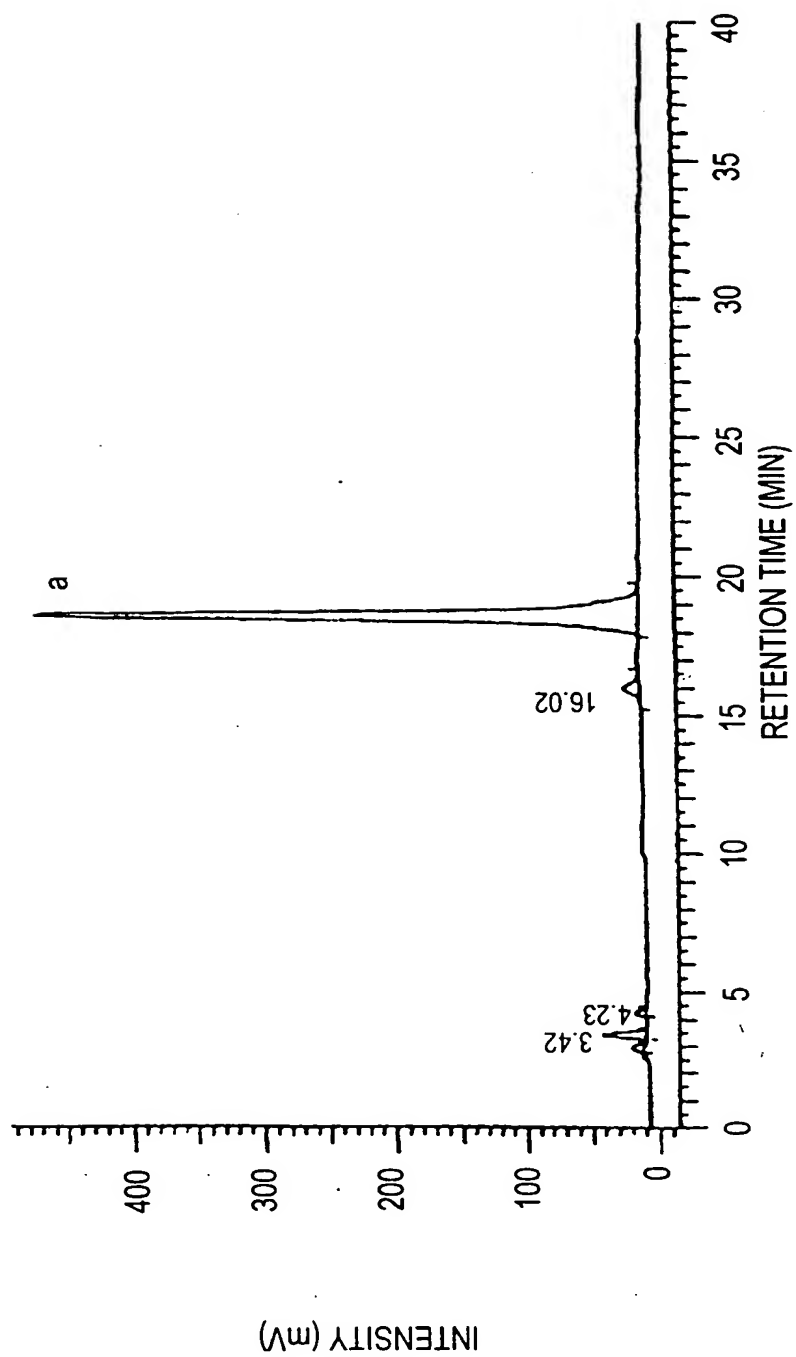


FIG. 7C

29/72

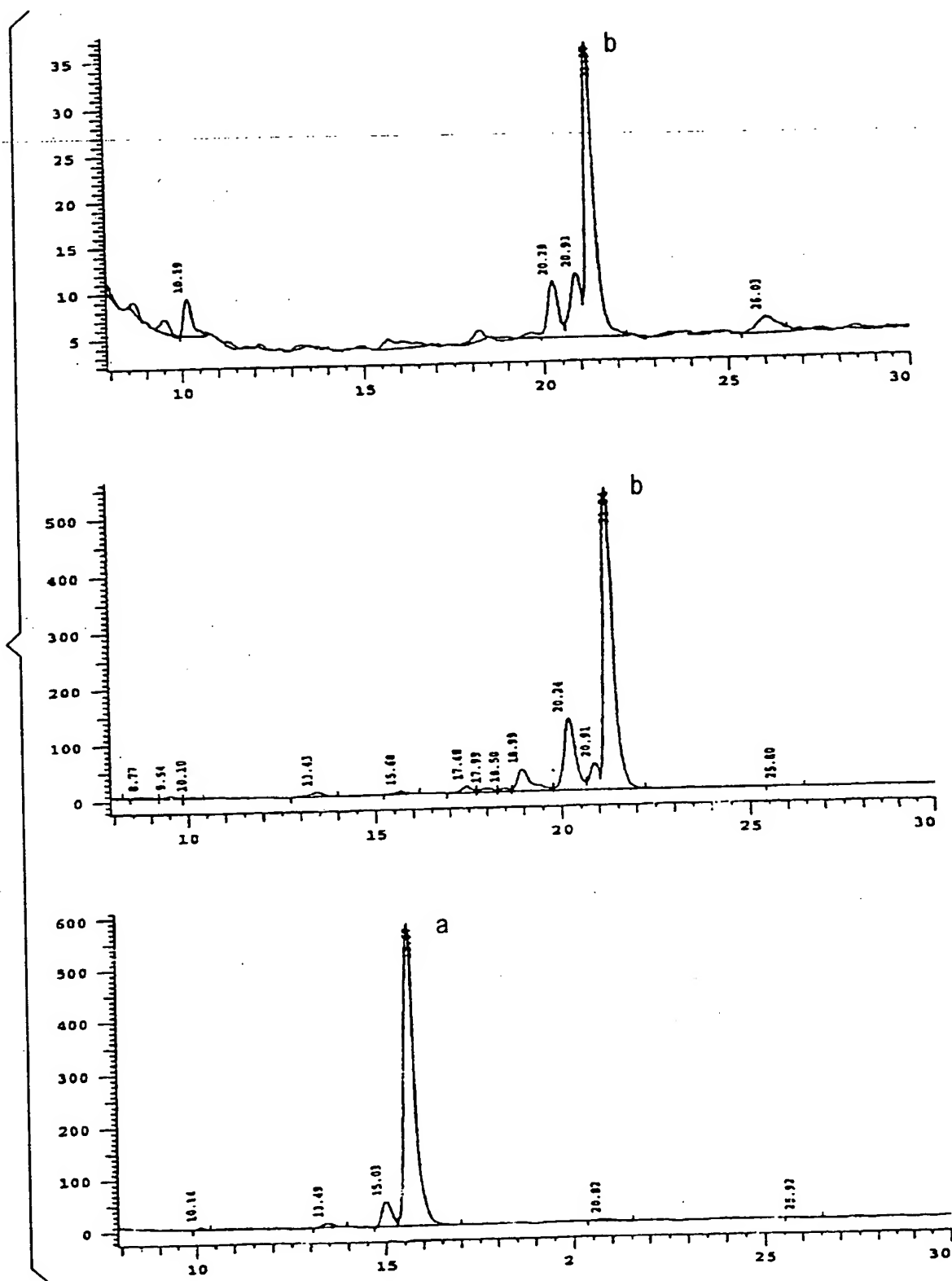


FIG. 8

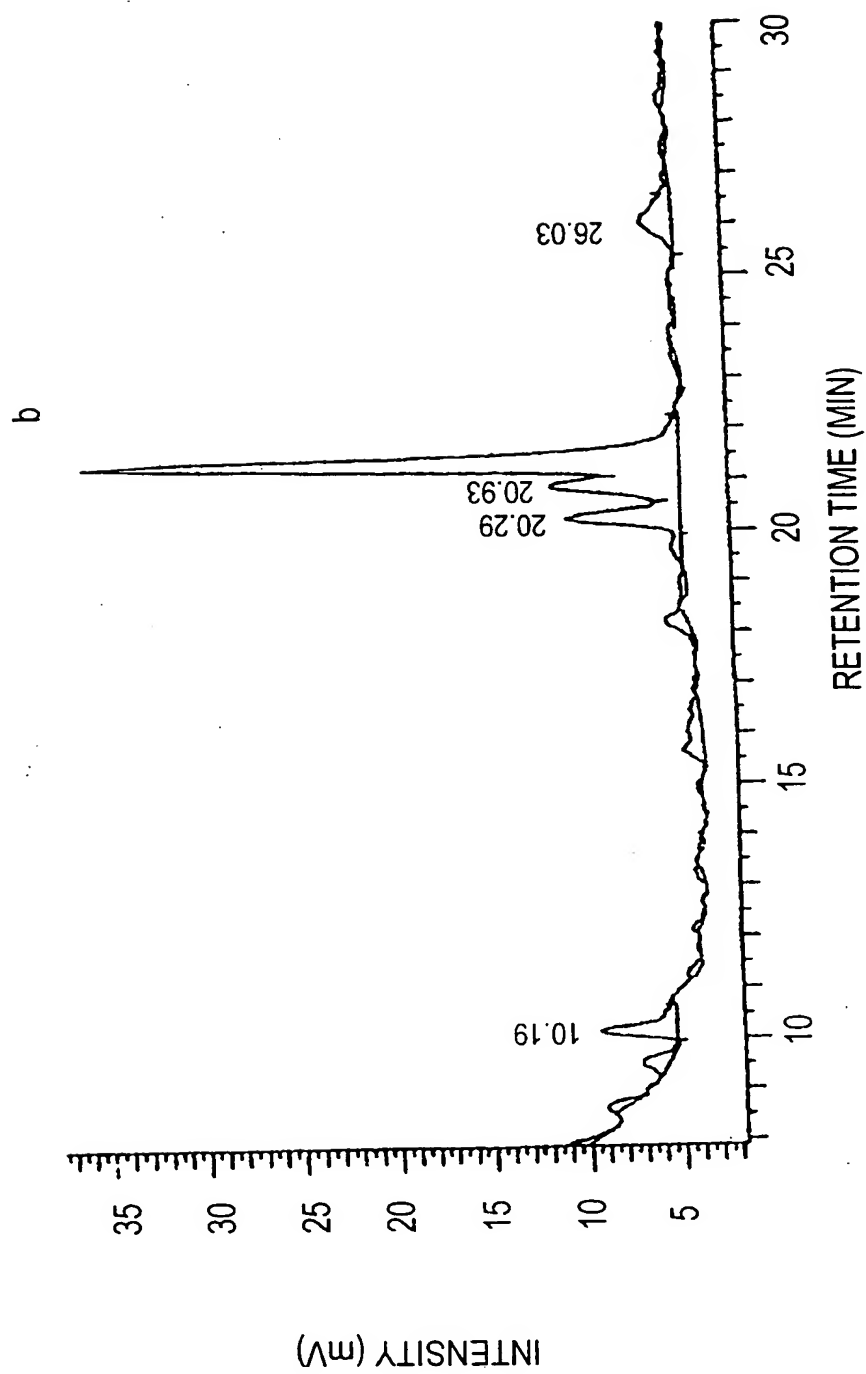


FIG. 8A

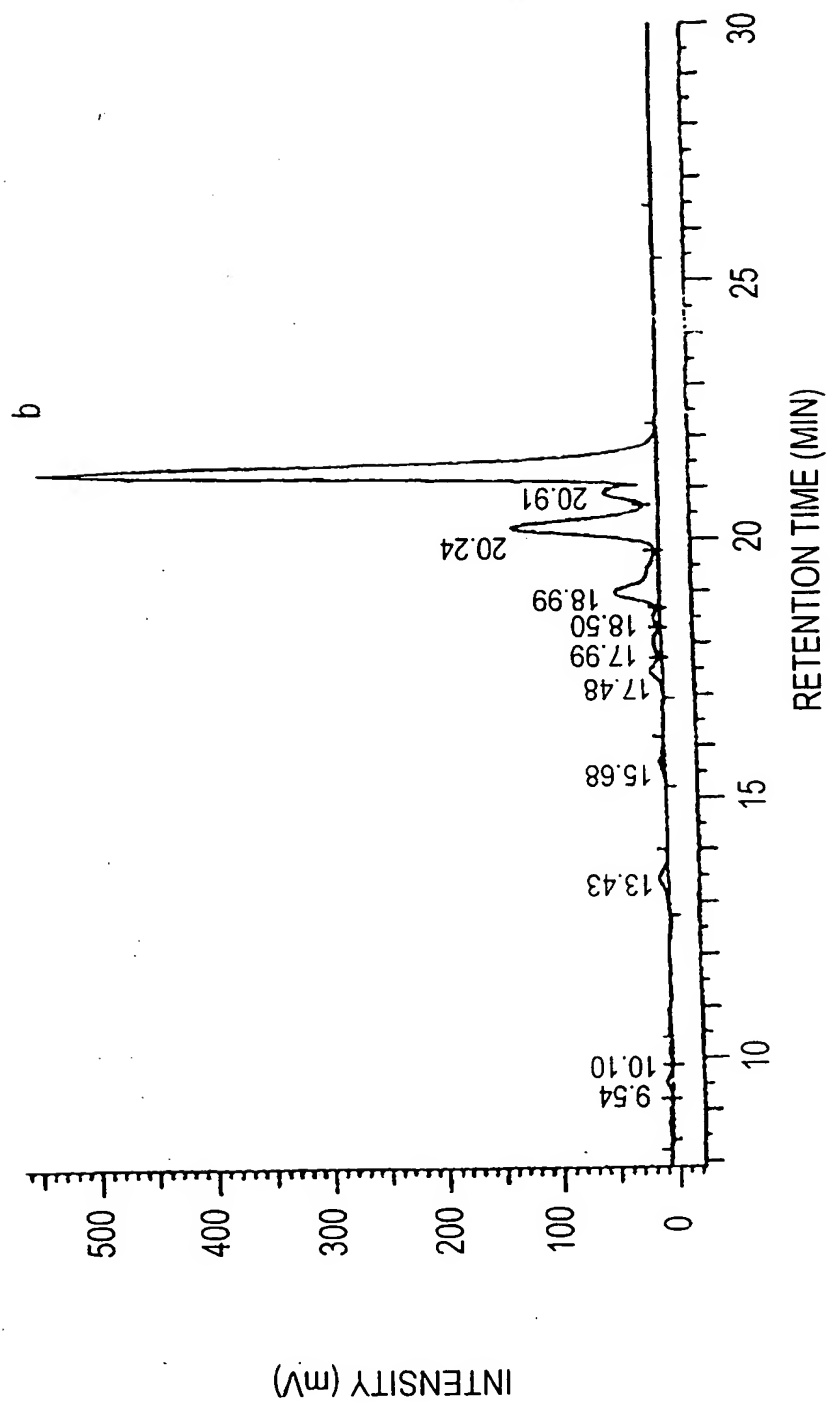


FIG. 8B

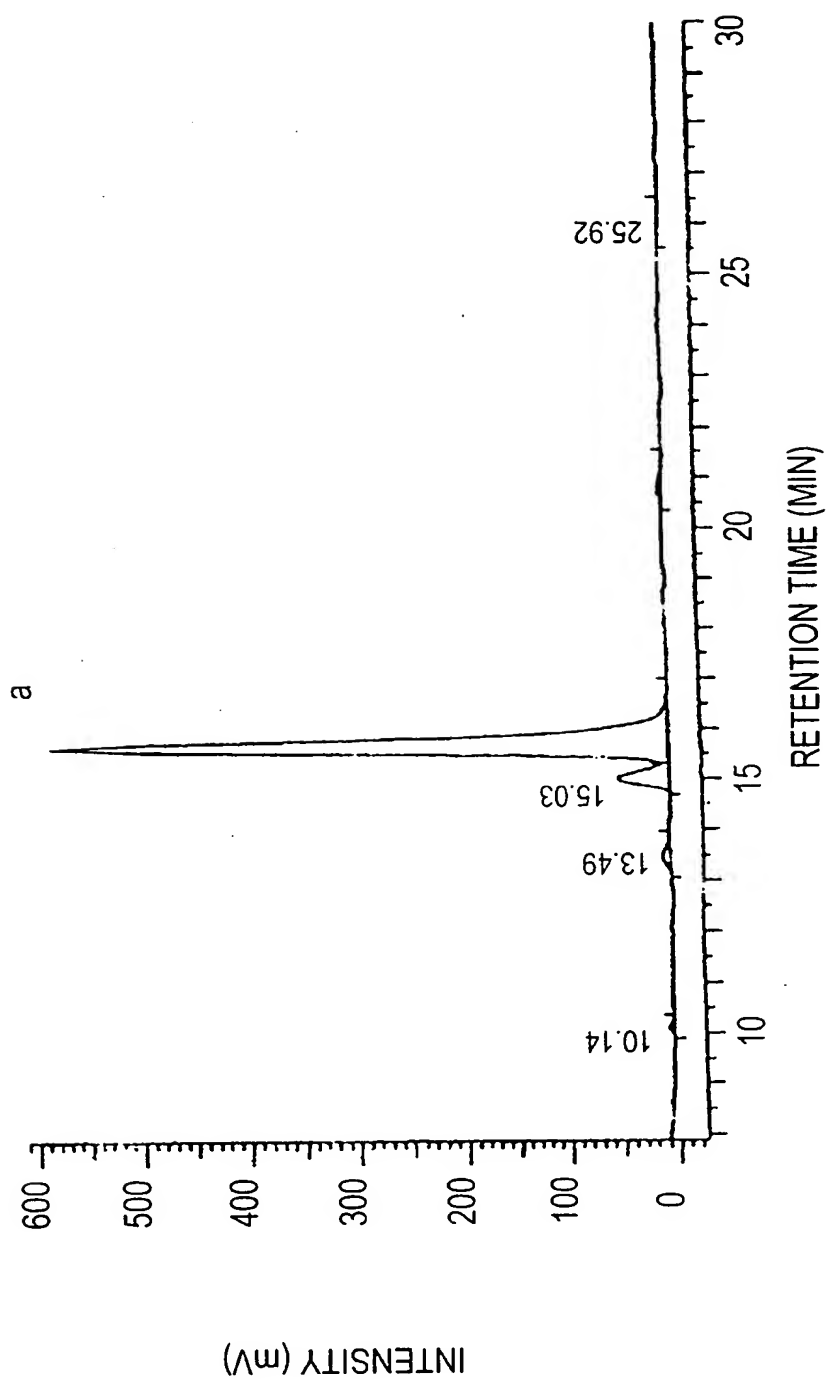


FIG. 8C

33/72

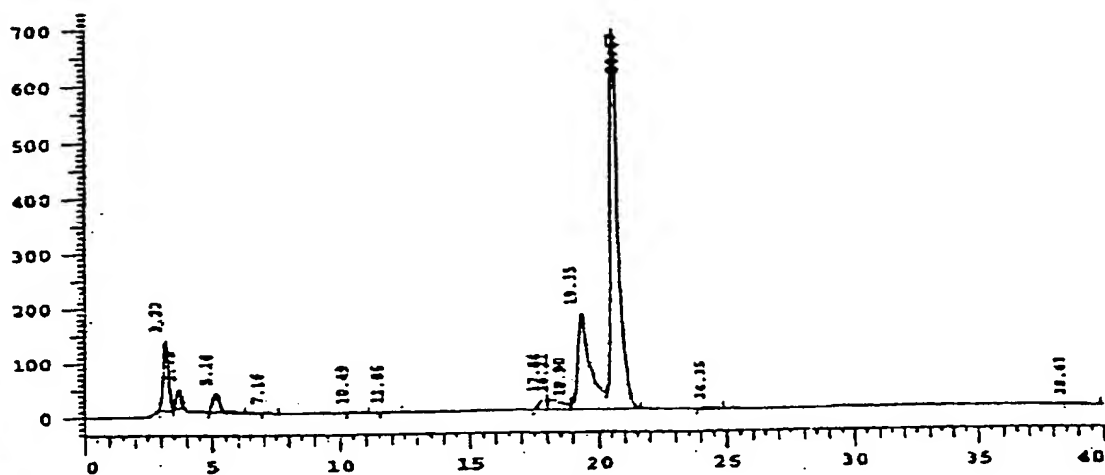
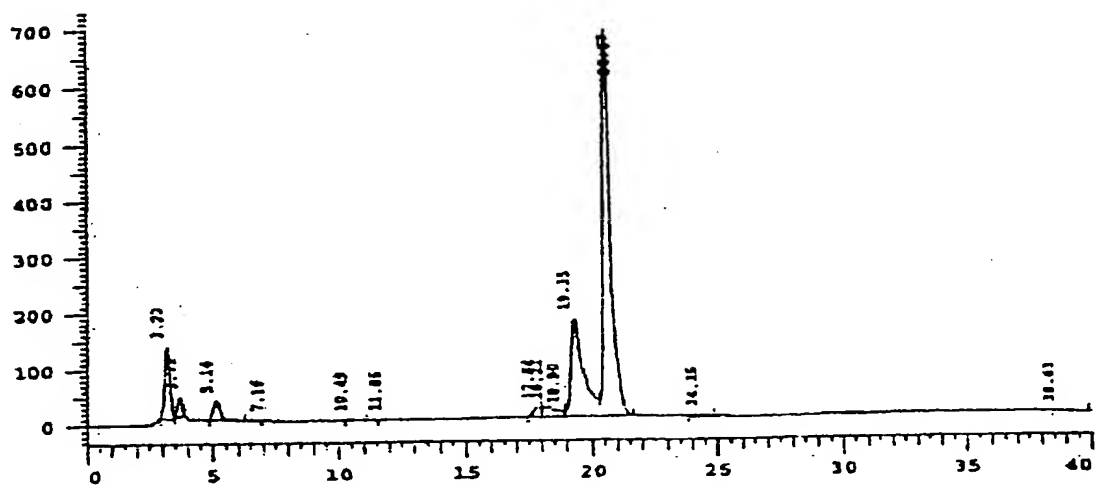
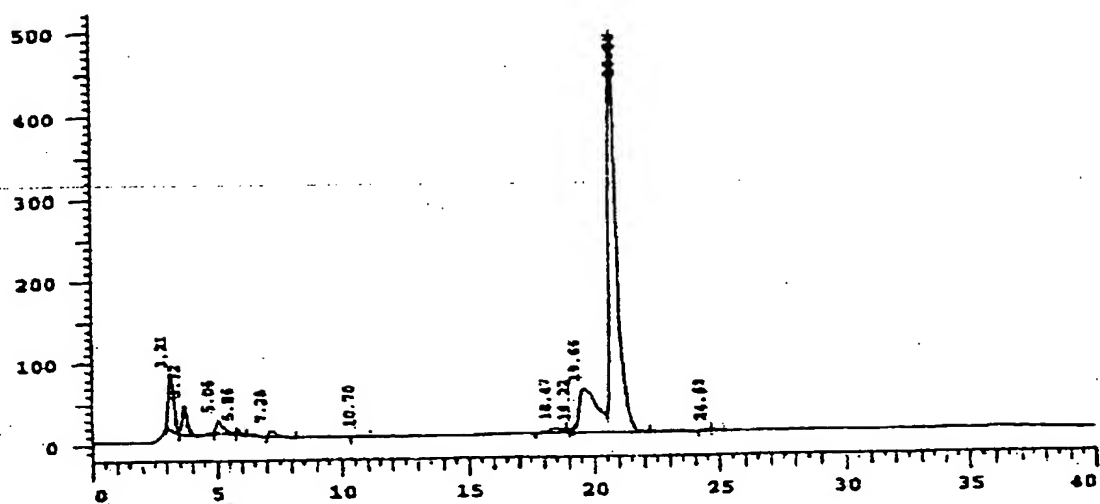


FIG. 9

34/72

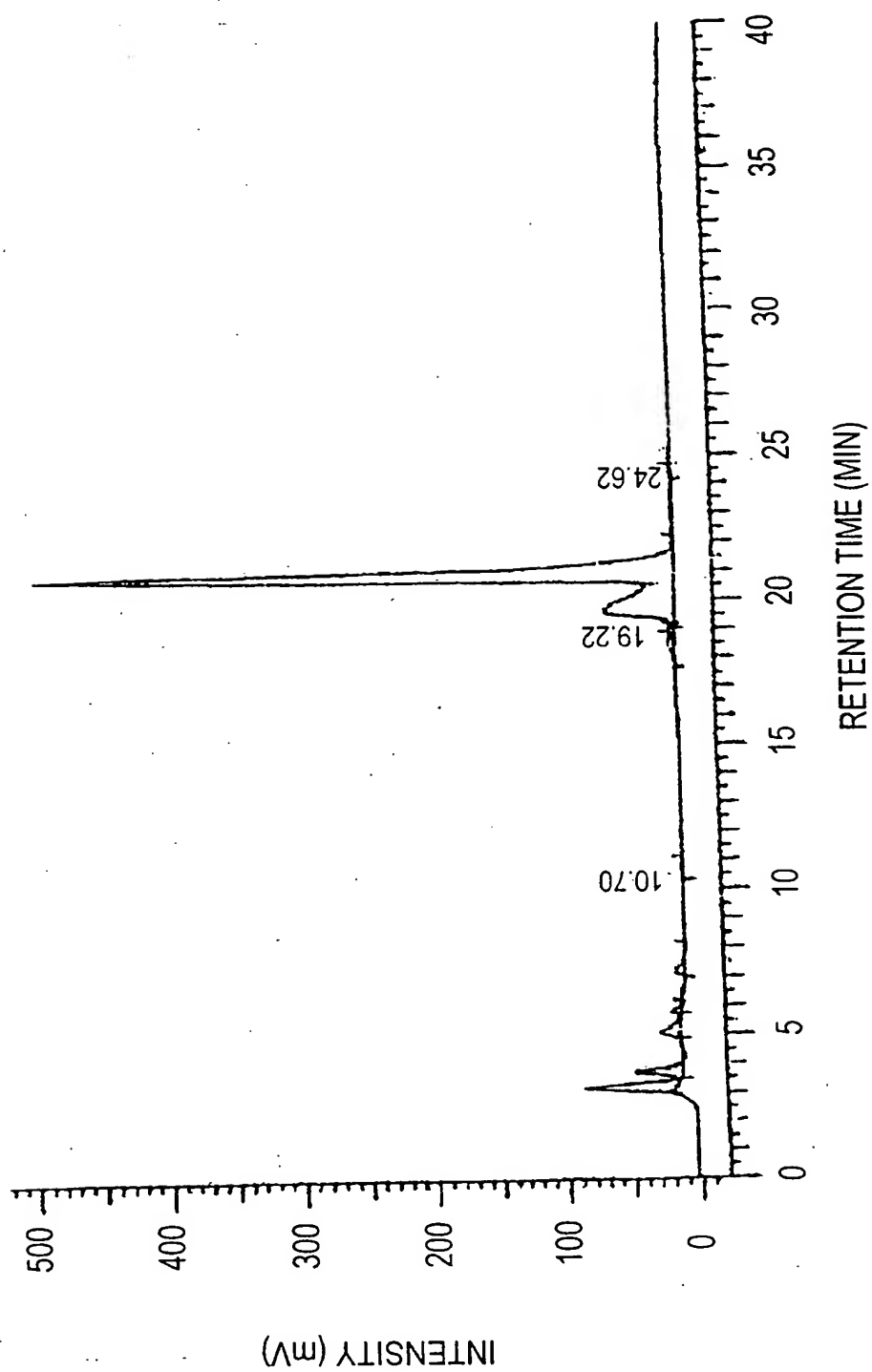


FIG. 9A

35/72

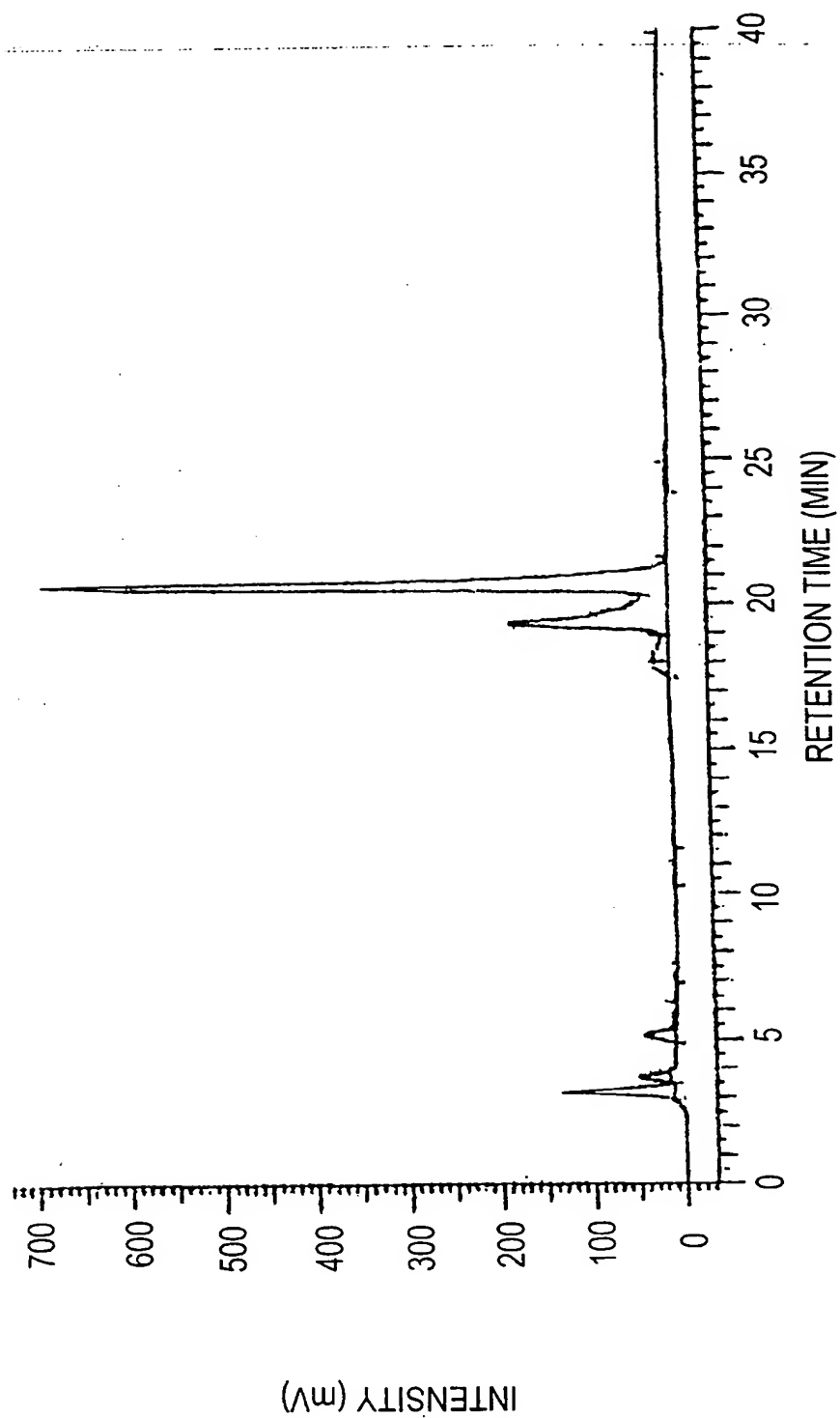


FIG. 9B

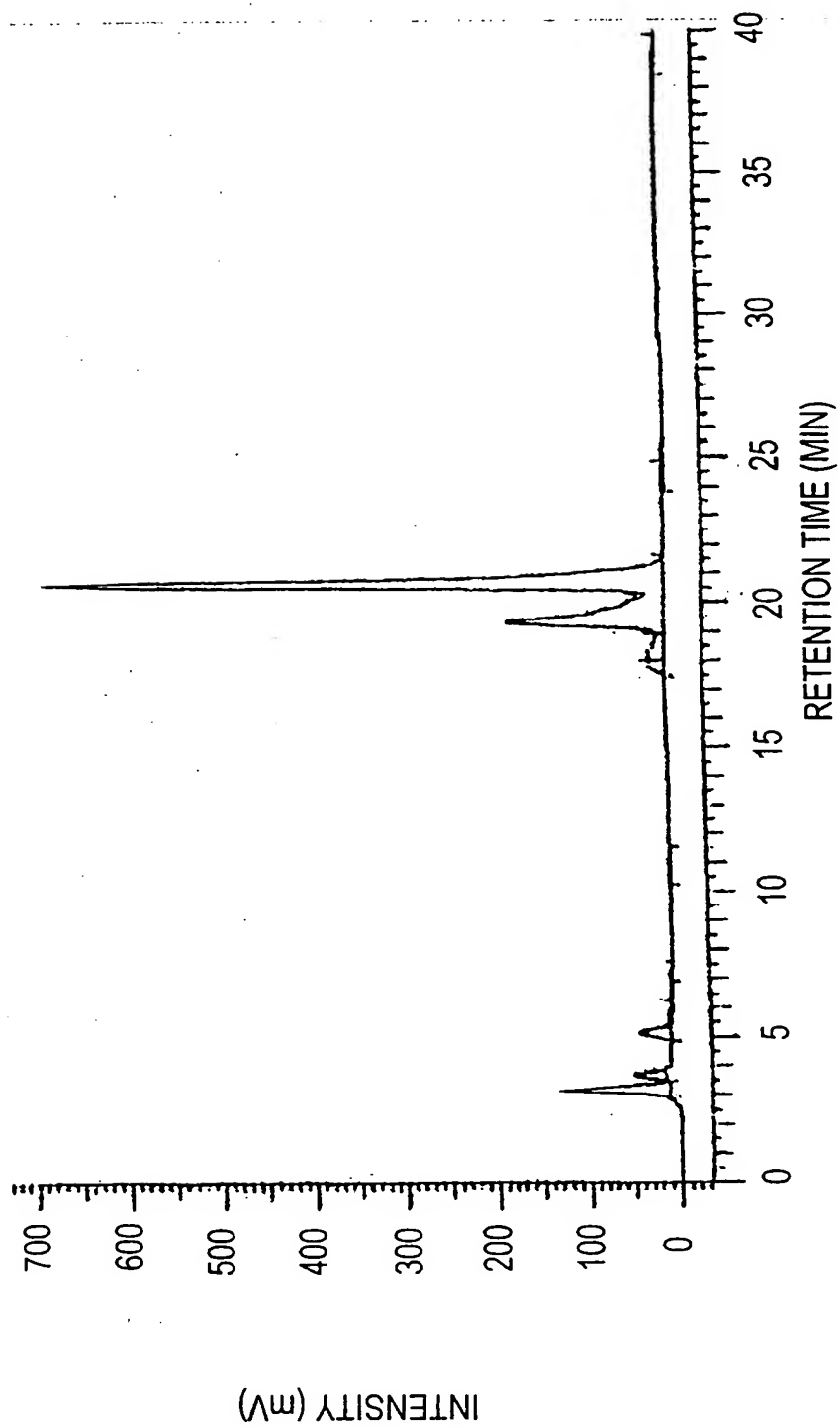


FIG. 9C

37172

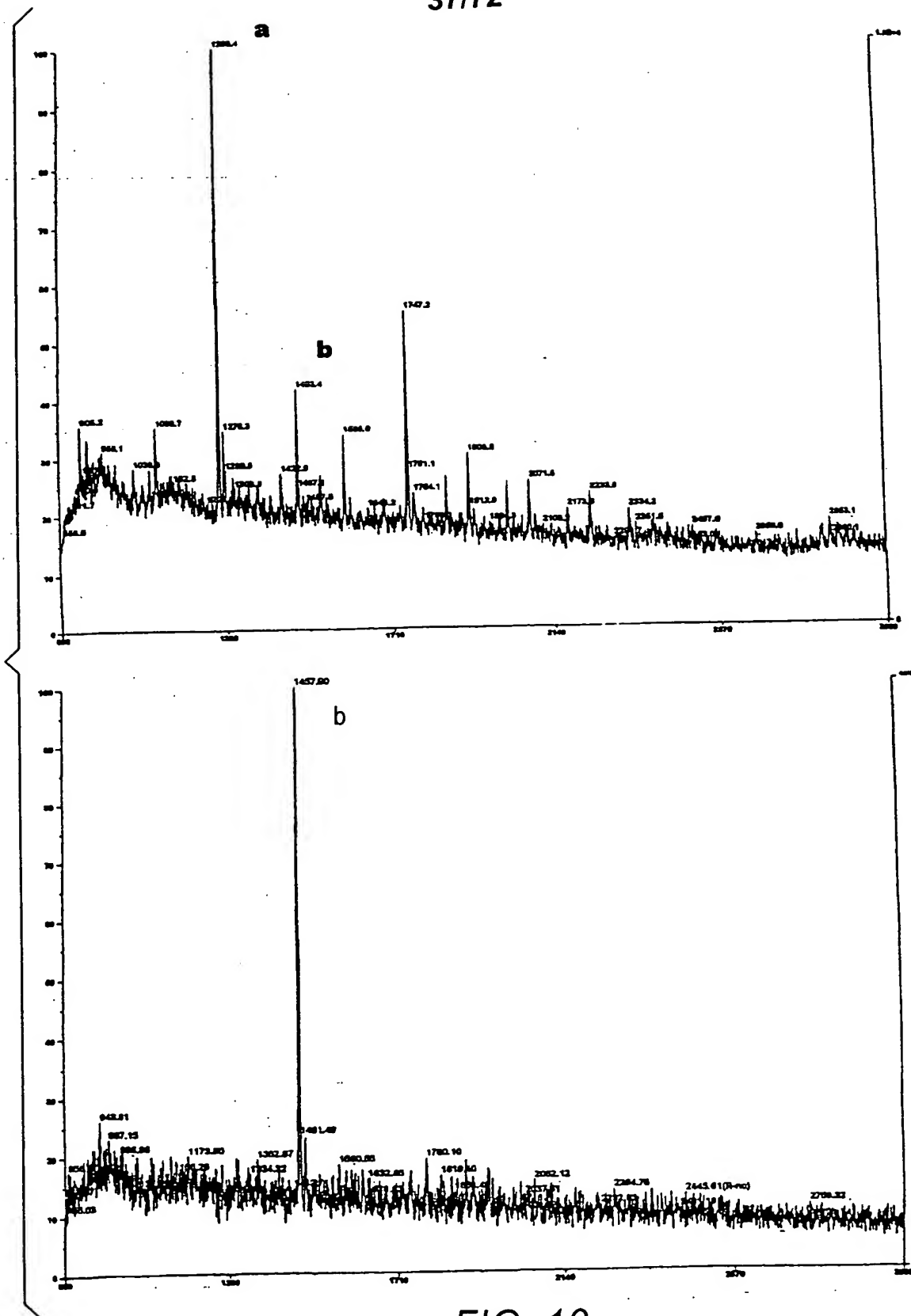


FIG. 10

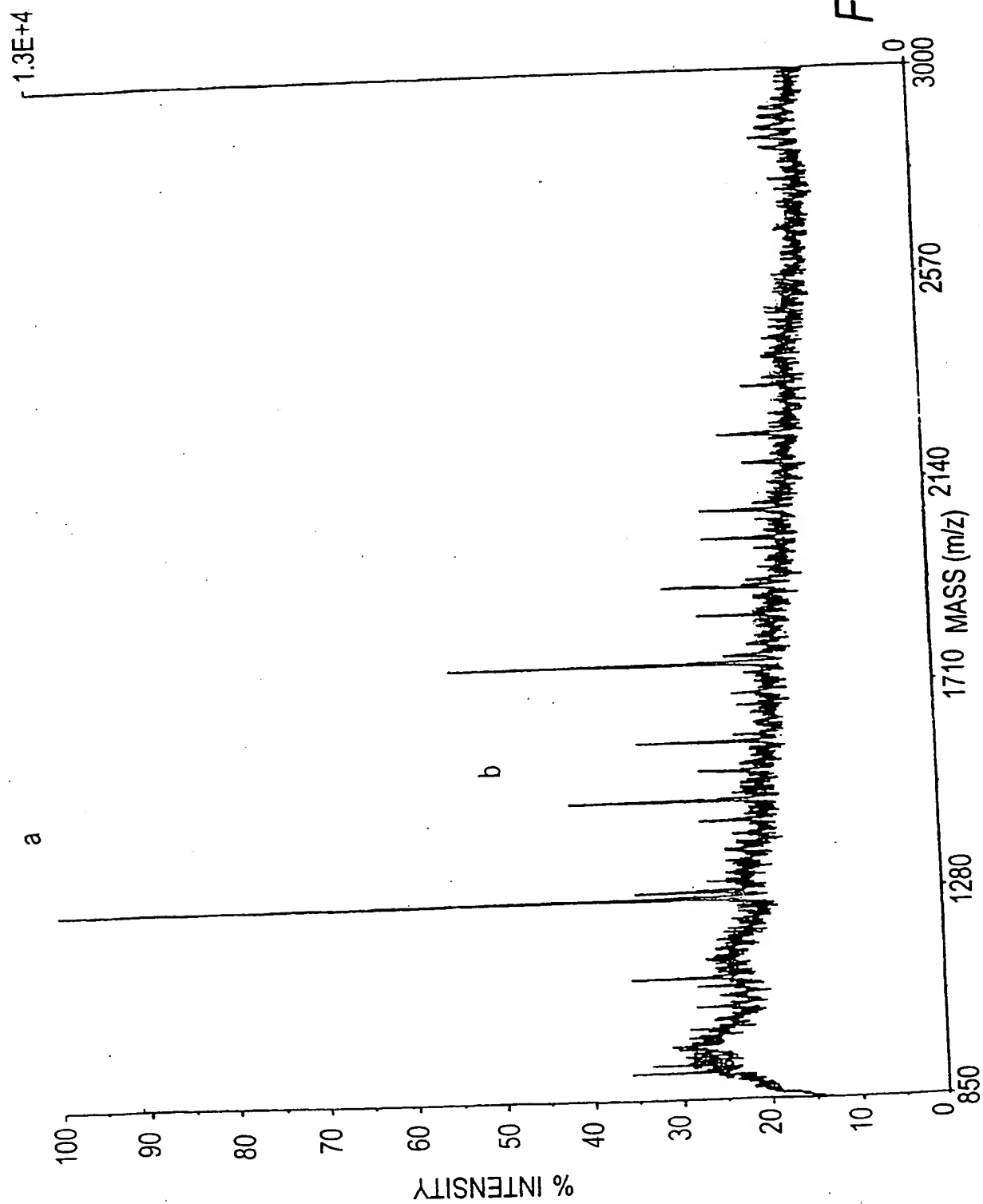


FIG. 10A

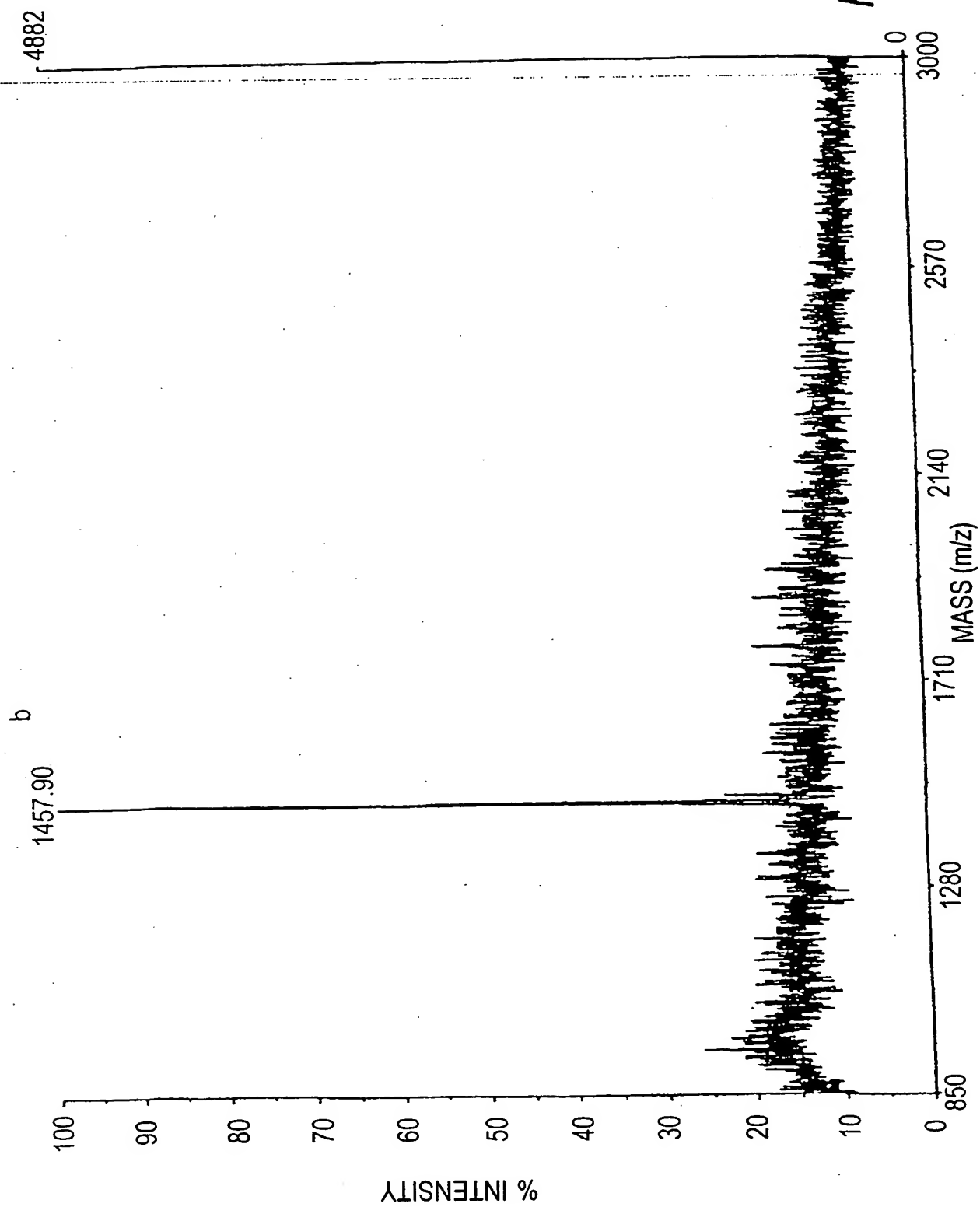


FIG. 10B

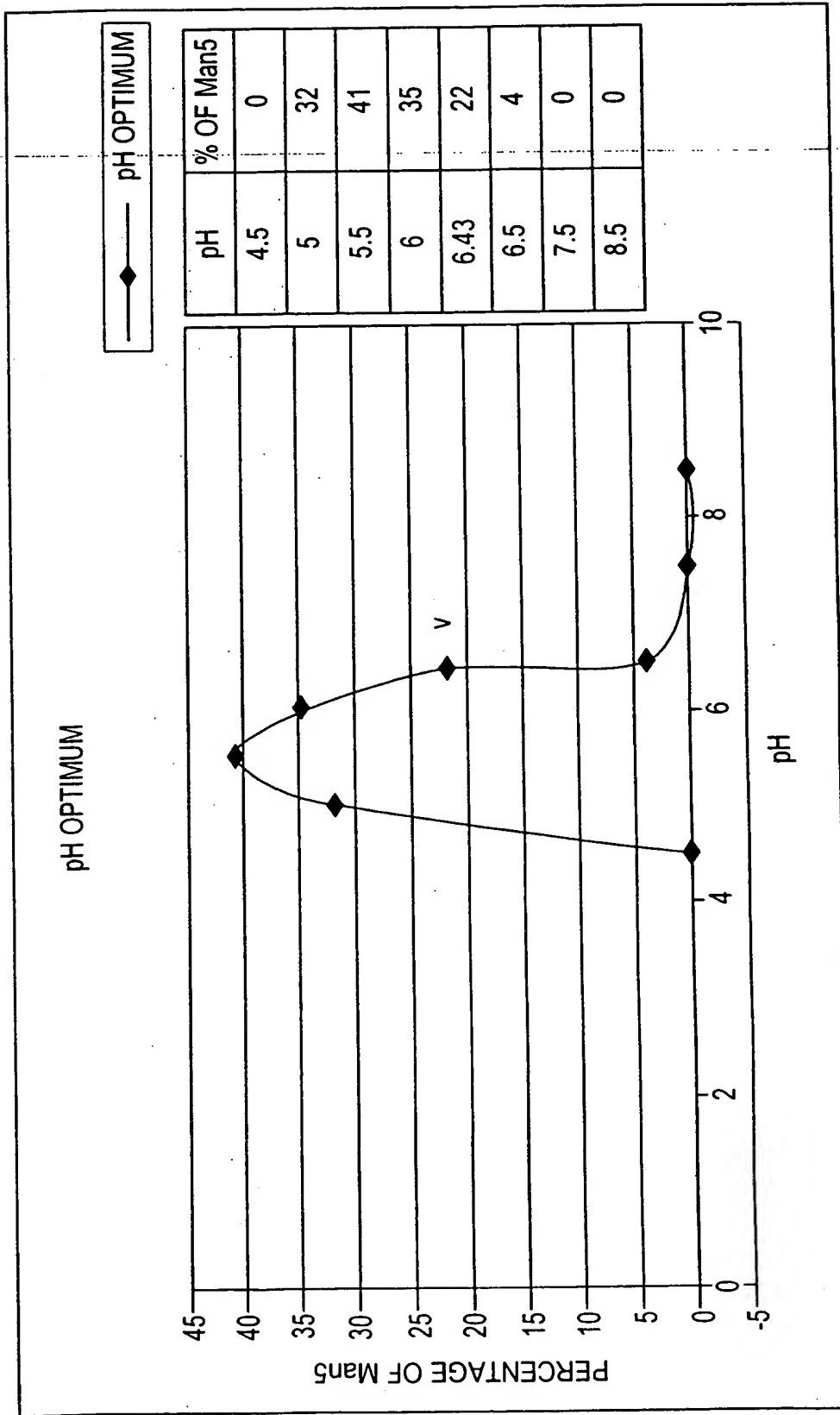


FIG. 11

41/72

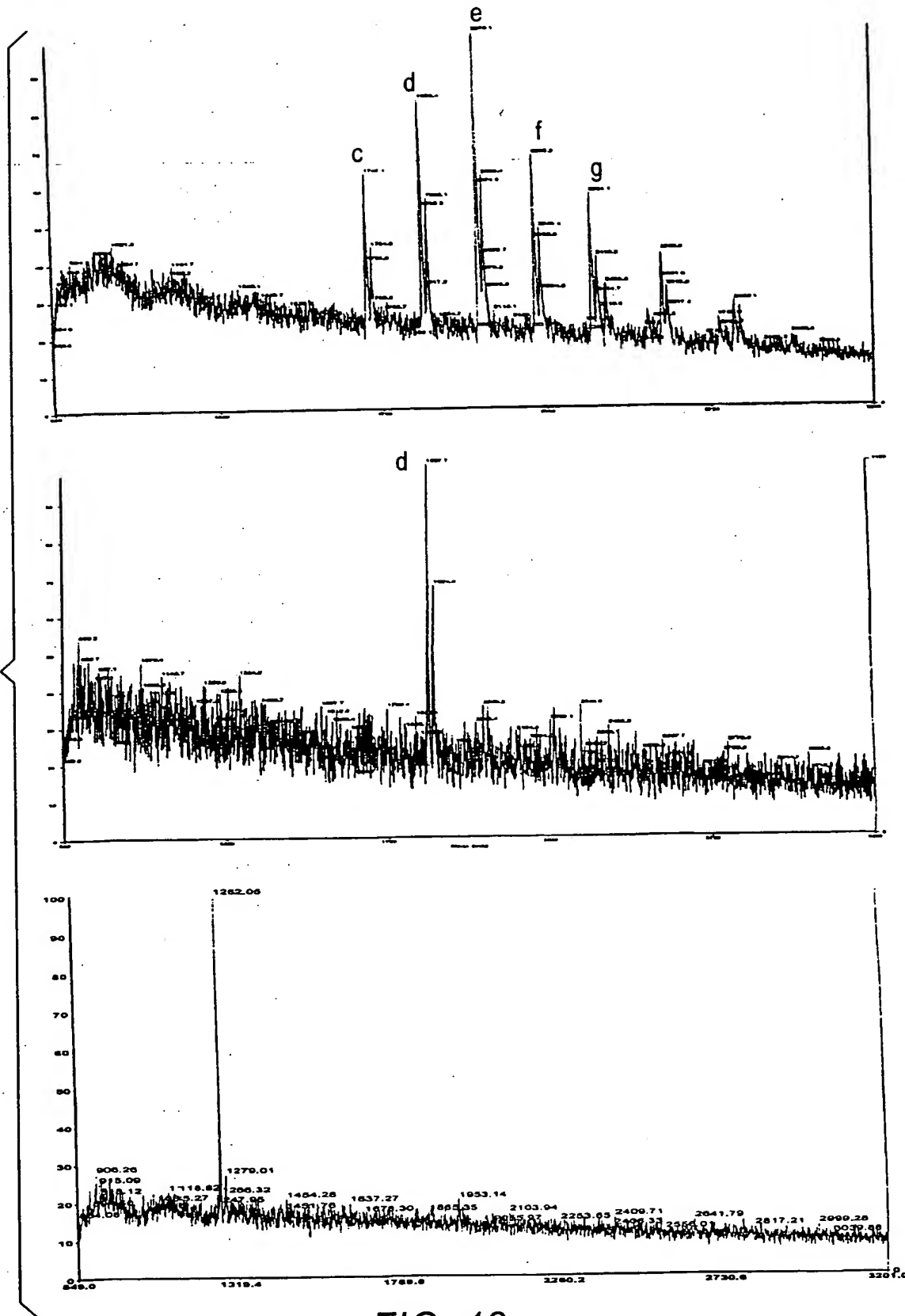
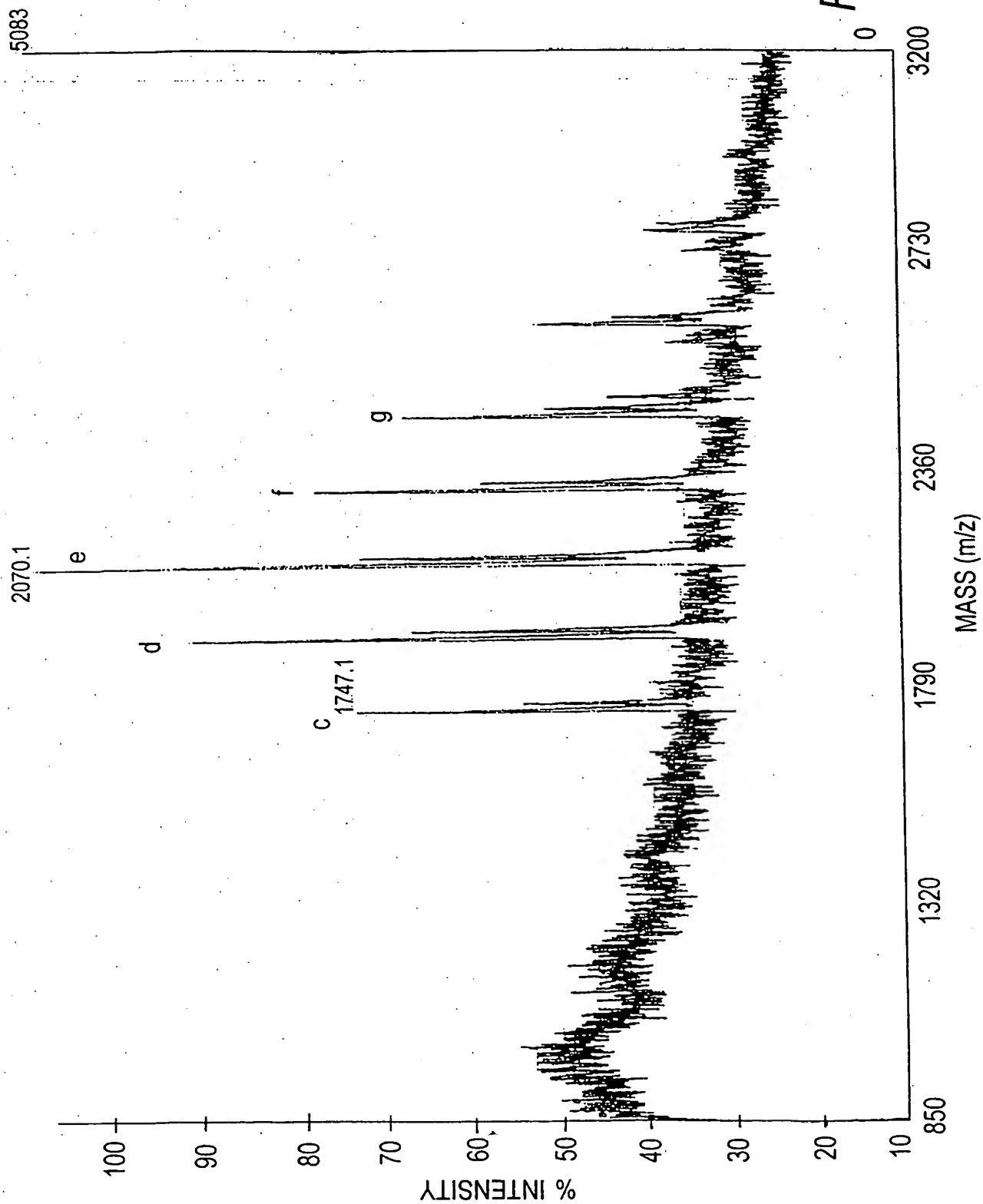
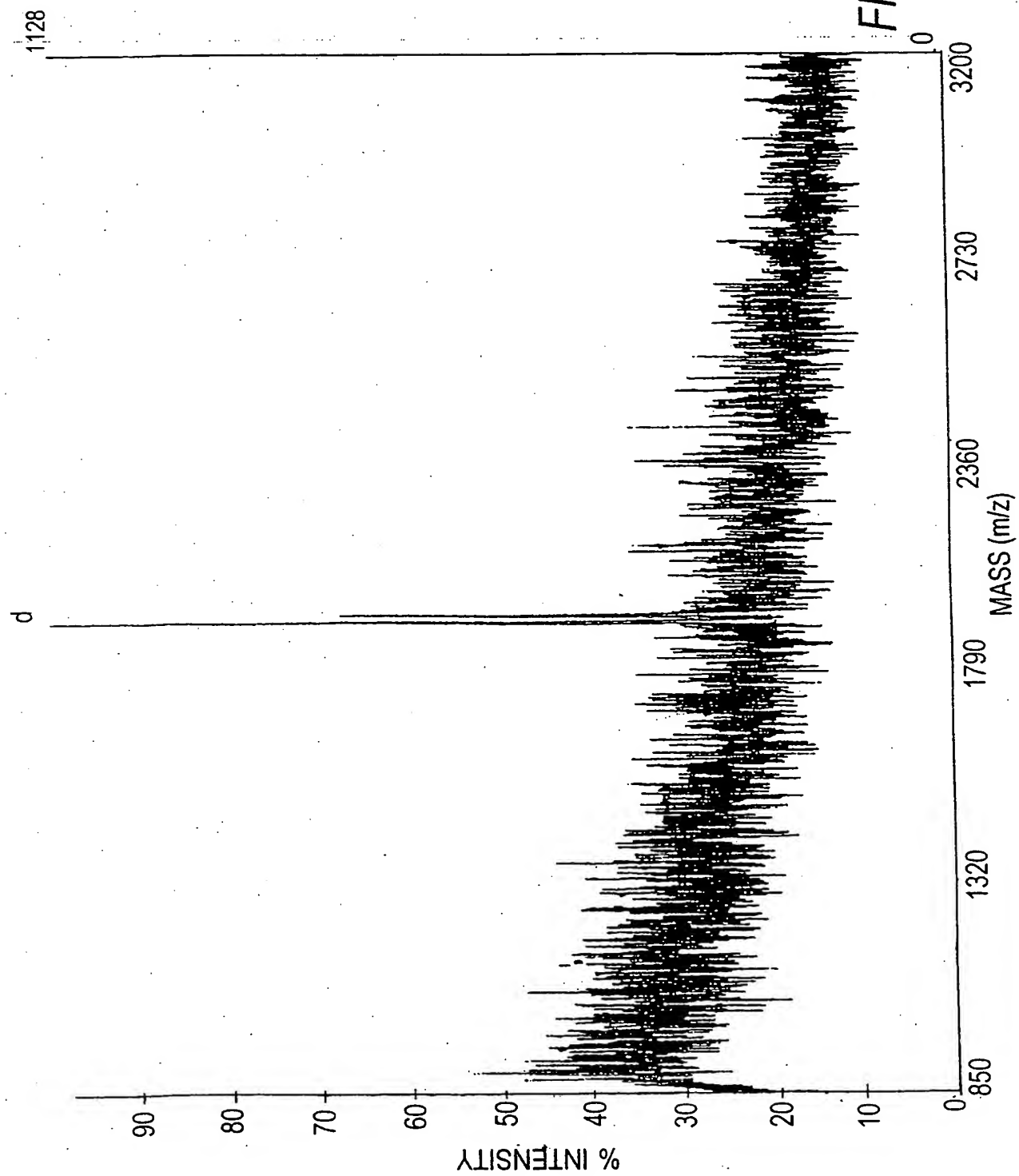


FIG. 12

42/72

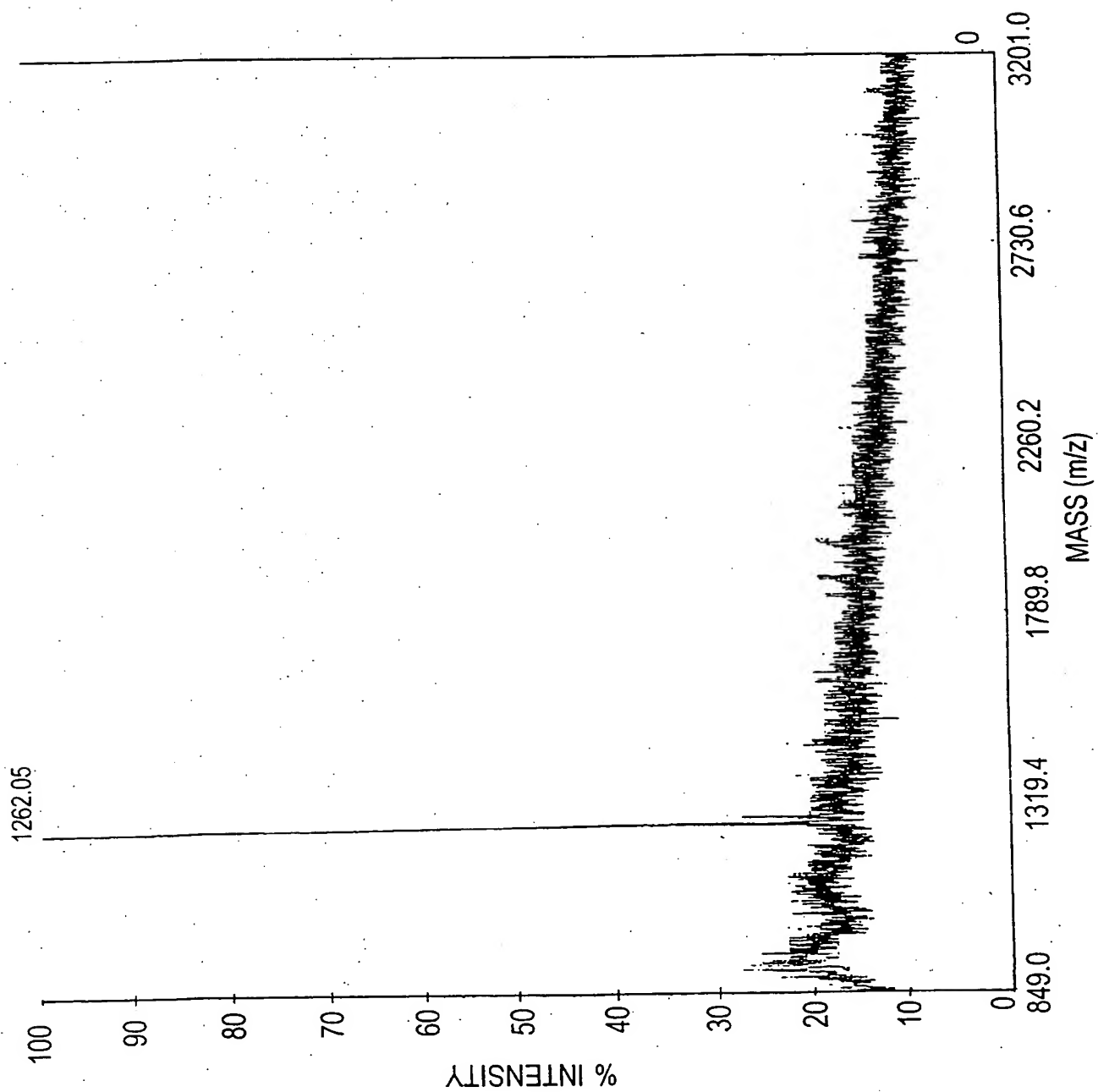


43/72



44/72

FIG. 12C



45/72

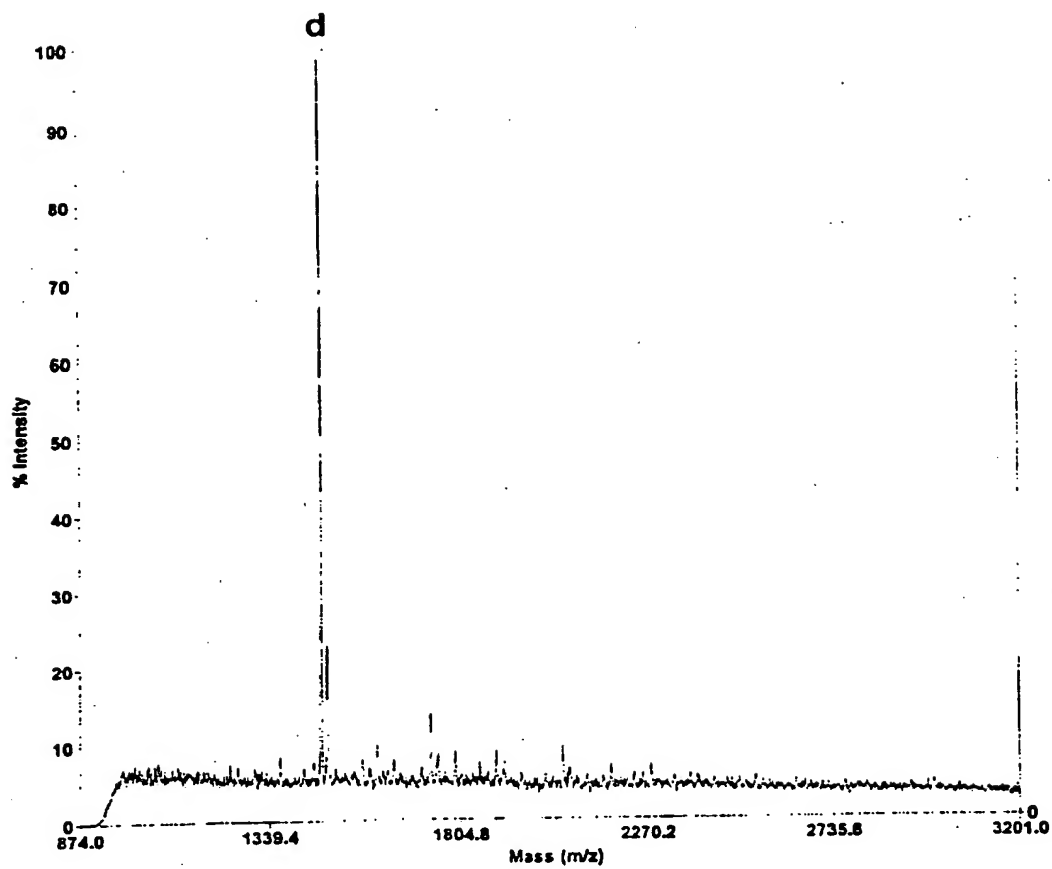


FIG. 13

46/72

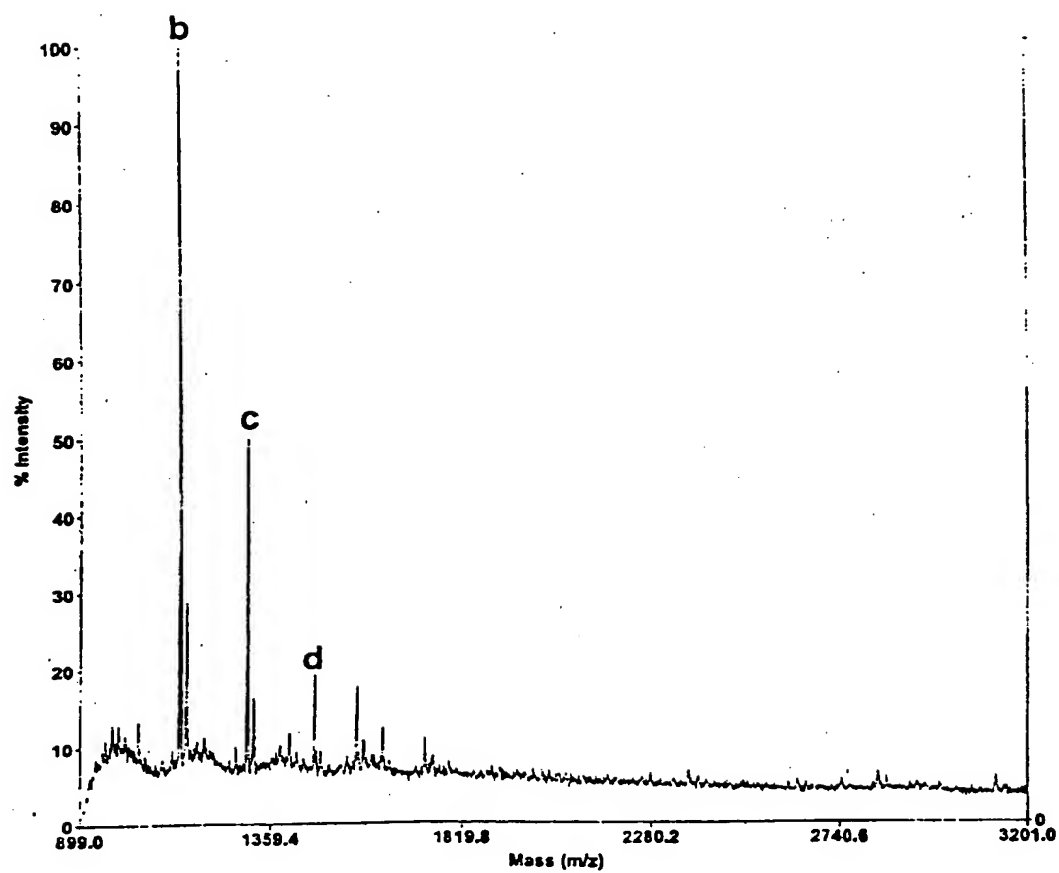


FIG. 14

47/72

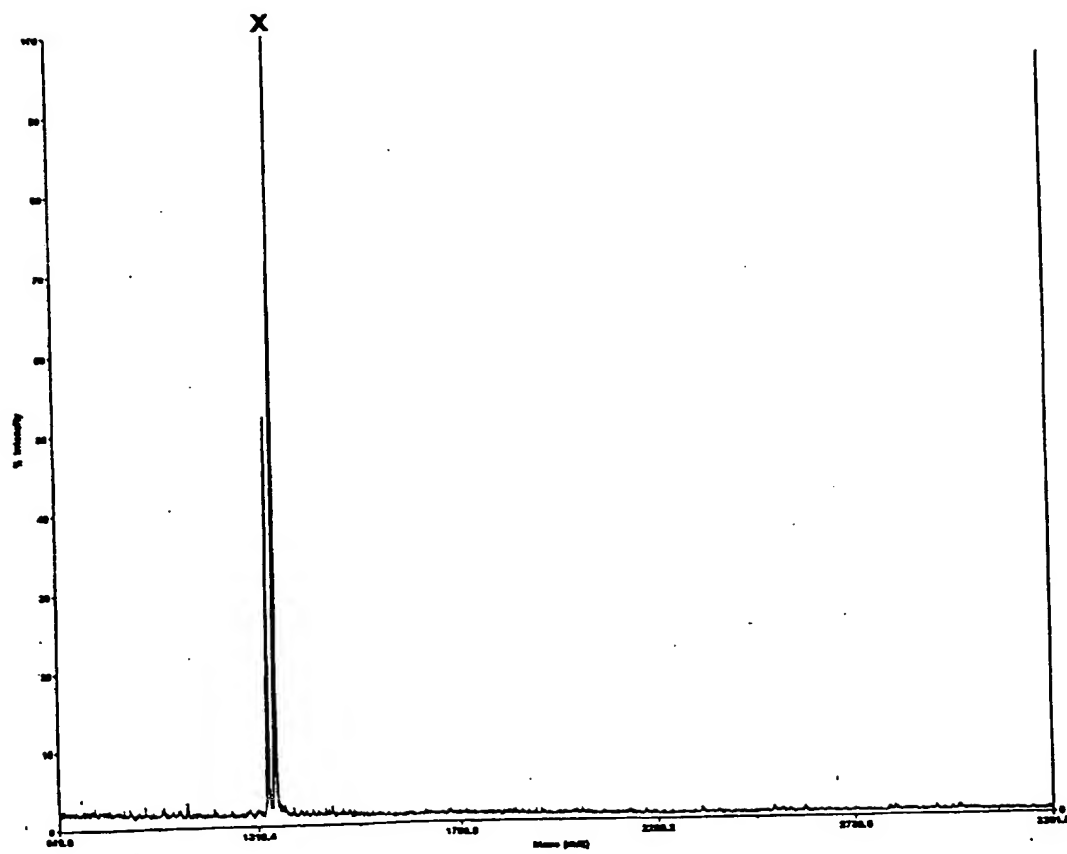


FIG. 15

48/72

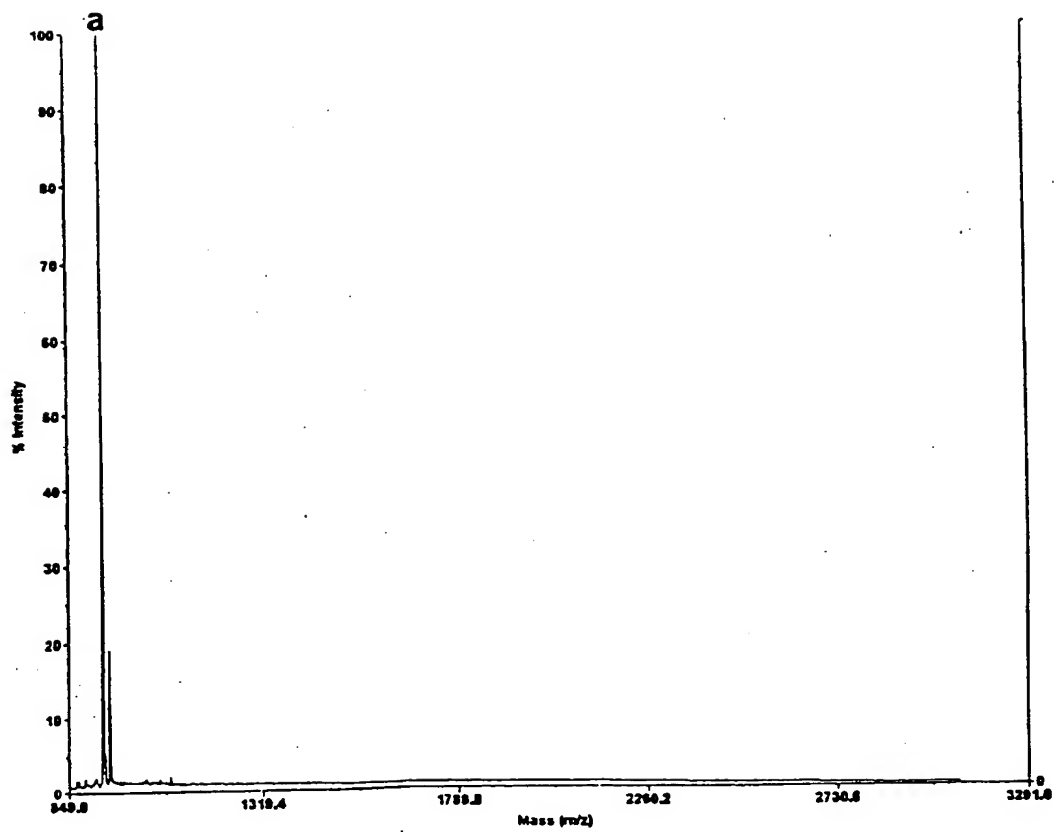
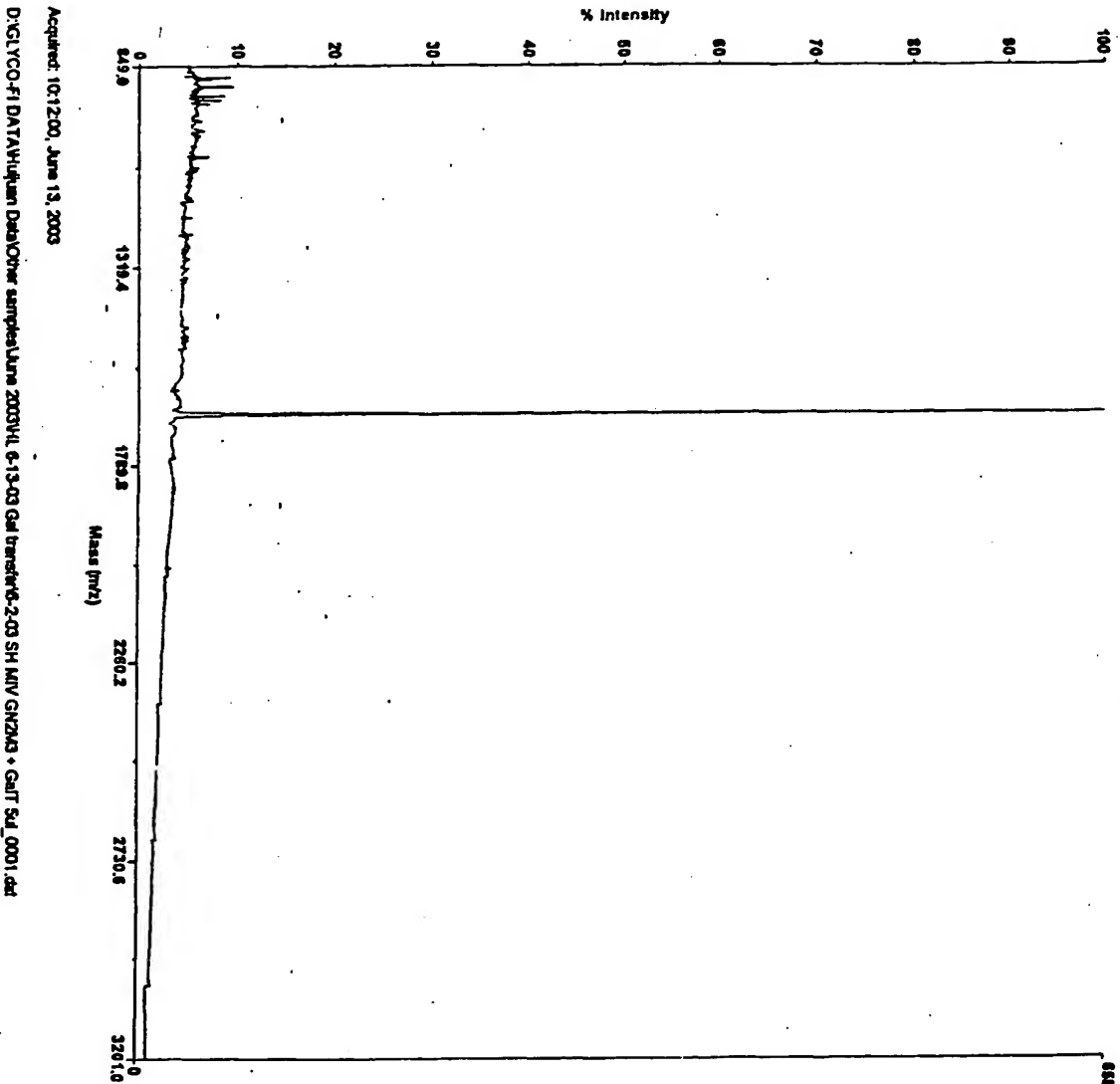


FIG. 16

Applied Biosystems Voyager System 1246

V. yager Spec #1246BC=NR(2.00)BP = 1664.6, 659]

FIG. 17



Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual

Accelerating voltage: 20000 V
Grid voltage: 84%
Guide wire Q: 0.05%
Extraction delay time: 100 msec

Acquisition mass range: 850 - 3200 Da
Number of laser shots: 1000/spectrum
Laser intensity: 2713
Laser Rep Rate: 20.0 Hz
Calibration type: Default
Calibration method: 2,5-Dihydroxyphenacetic acid
Low mass gate: 800 Da

Digitizer start time: 18.582
Bin size: 2 msec
Number of data points: 8676
Vertical scale: 500 mV
Vertical offset: 0%
Input bandwidth: 150 MHz

Sample well: 47
Plate ID: 100 WELL PLATE
Serial number: 1246
Instrument name: Voyager-DE
Plate type filename: C:\VOYAGER\100 well plate.pl
Lab name: PE Biosystems

Absolute x-position: 31305.6
Absolute y-position: 28069.3
Relative x-position: -761.813
Relative y-position: 1081.83
Spots in spectrum: 100
Source pressure: 4.38e-007
Mirror pressure: 0
TC2 pressure: 0.00453
TIS gate width: 30
TIS flight length: 9.40

Printed: 08:41, June 16, 2003

Milestone V. yager

50/72

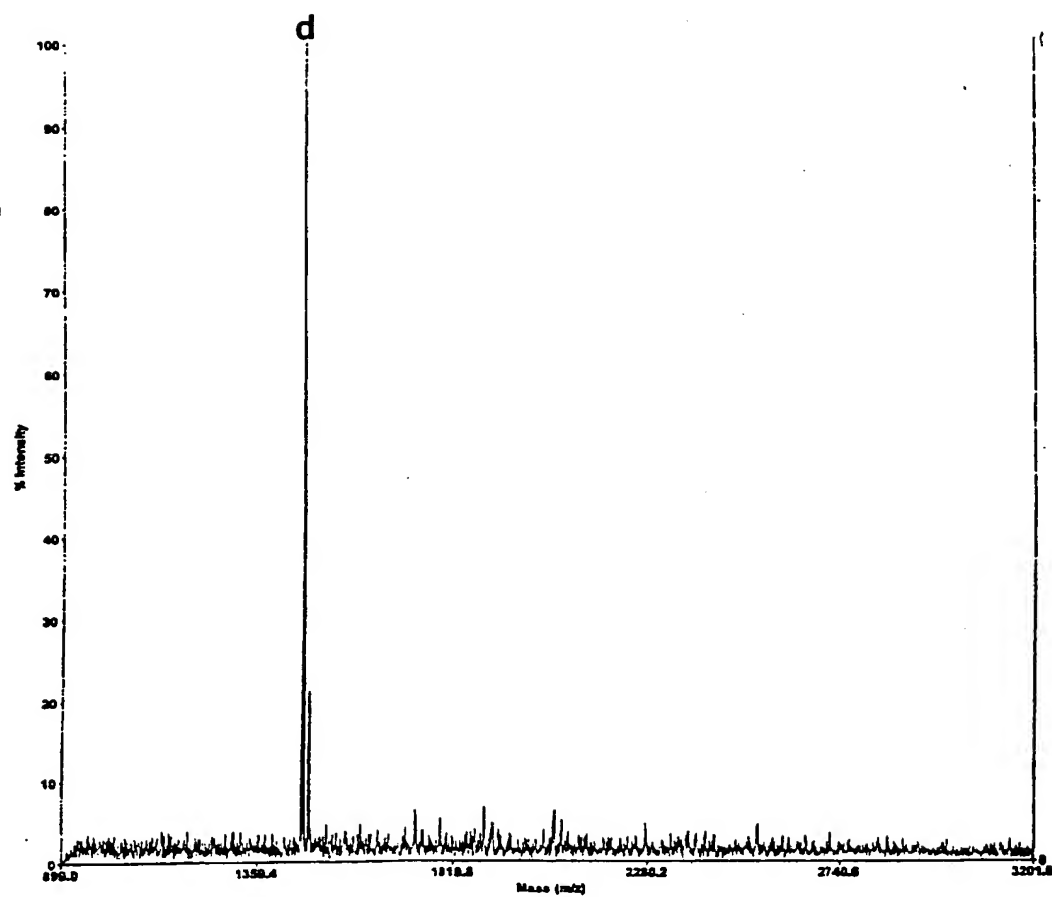


FIG. 18

51/72

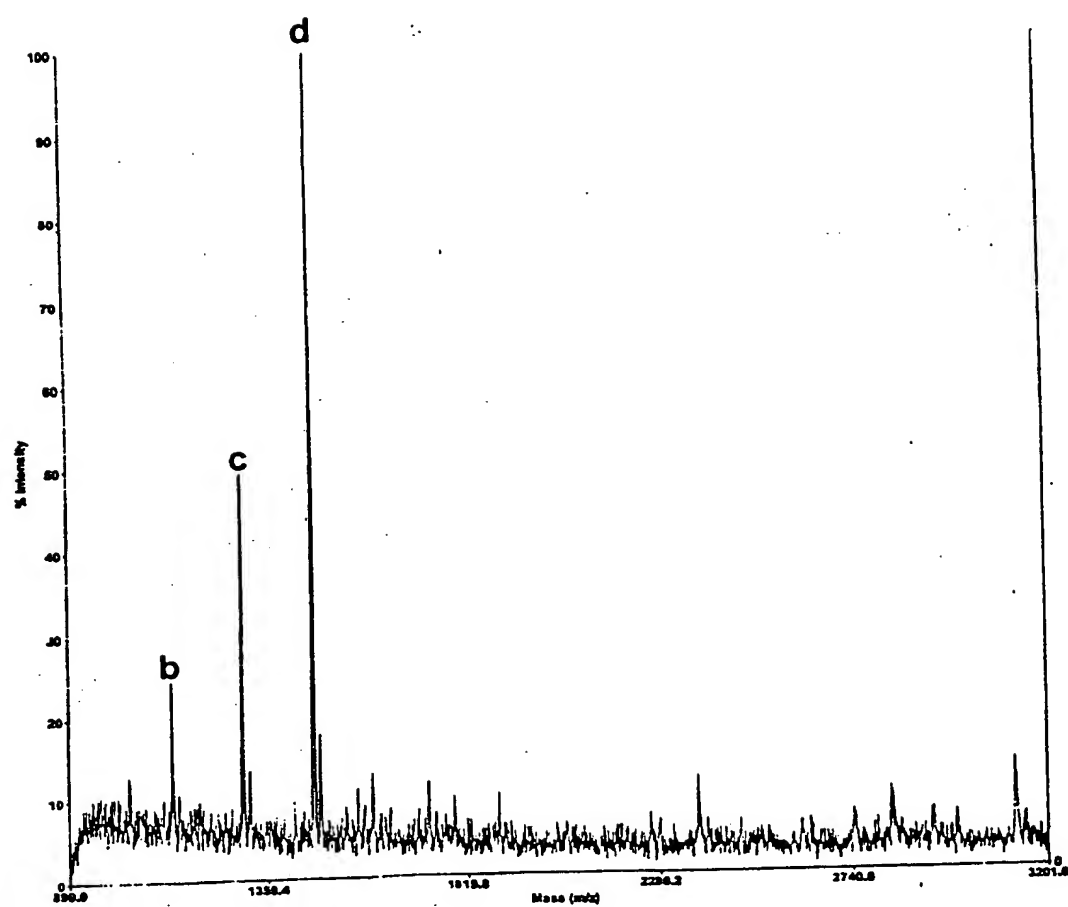


FIG. 19

52/72

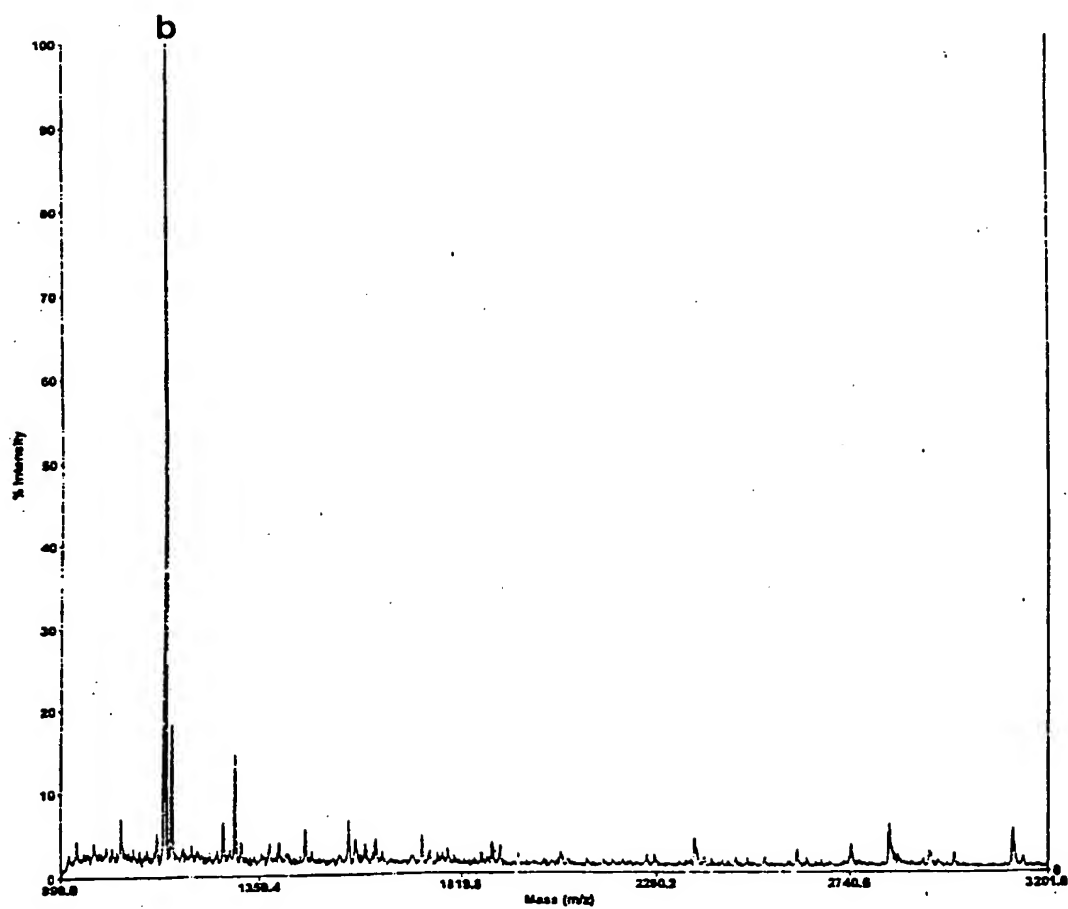


FIG. 20

53/72

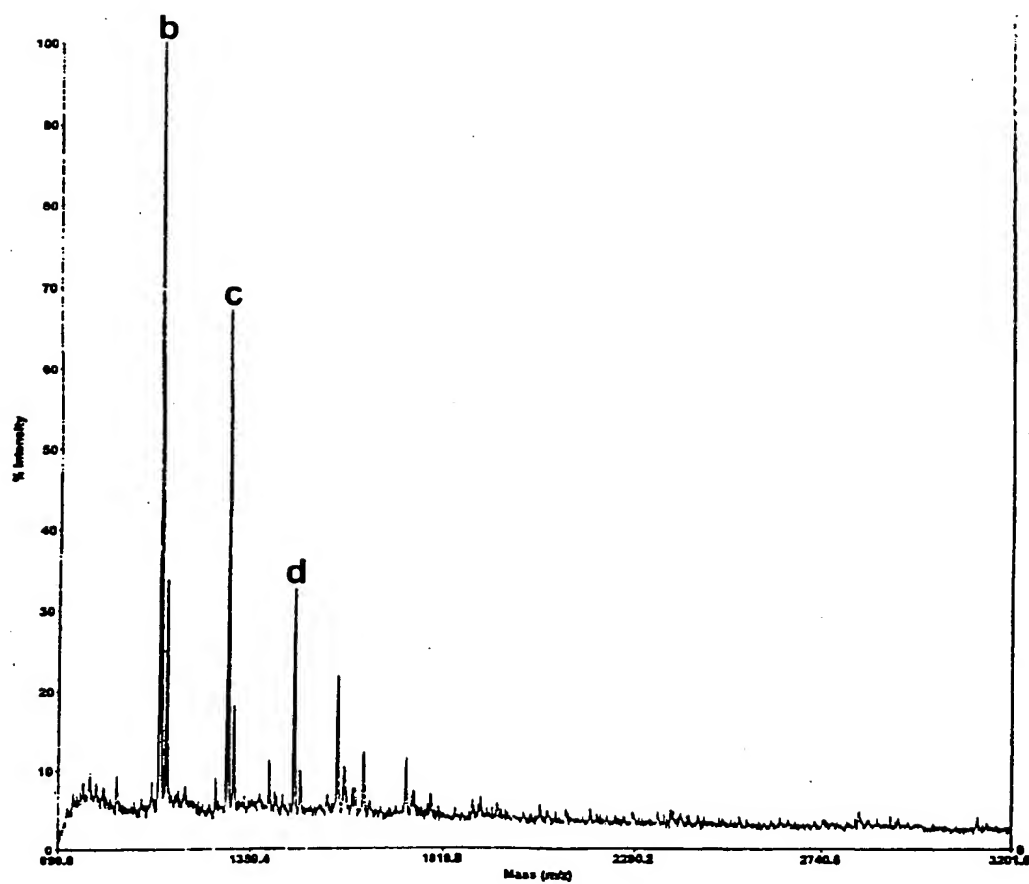


FIG. 21

54/72

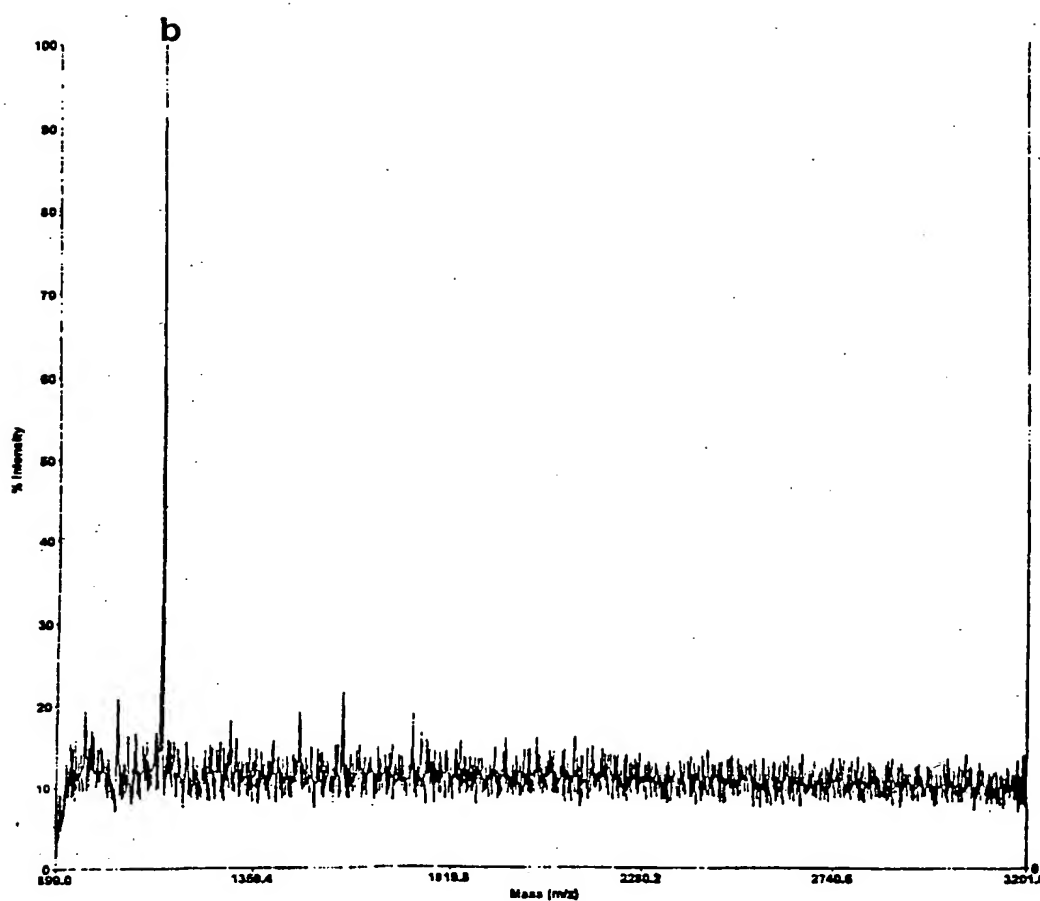
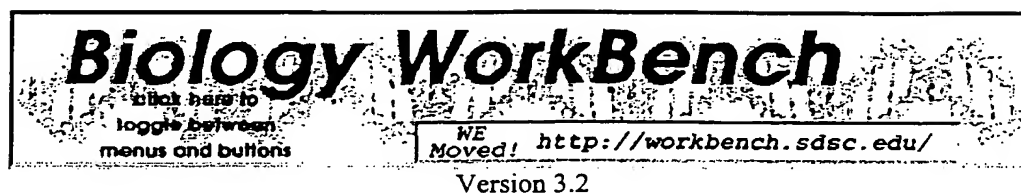


FIG. 22



BOXSHADE
Color-Coded Plots of Pre-Aligned Sequences

Selected Sequence(s)
• Droso MannII (X77652),
C.elegans MannII,
rMannII (XM_218816.1),
hMannIIx D55649,
Mouse MannII (X61172),
human MannII (U31520),
CionaMannII (AK116684),
ArabMannII,
Insect ManIII,
hLyso MannII,
hCyto MannII (NM_006715)



FIG. 23

Download a PostScript version of the output

```

Droso_MannII_[X] 1 -----
C.elegans_MannI 1 -----
rMannII_[XM_218 1 MACIGGAQGGQQAVERKEPSHQGYPMWPMTHGSCSELALLSSTRMYCHQGCVRPPPTDVKN
hMannIIx_D55649 1 -----
Mouse_MannII_[X 1 -----
hMannII 1 -----
CionaMannII_[AR 1 -----
ArabMannII 1 -----
Insect_ManIII 1 -----
hLyso_MannII 1 -----
hCyto_MannII_[N 1 -----

Droso_MannII_[X 1 -----M-----VICSGCLVPLISLYIMFAAP-----AATQIRP
C.elegans_MannI 1 -----MGR-----ILCLG-VPLTVSLTYXGIETG-----AEALTRR
rMannII_[XM_218 61 PRTTDTQSVPGVSY-----CGAAIFCAVTSITMDRVOHDPAR-BQNGGNYPPRS
hMannIIx_D55649 1 -----M-----CGAAIFCAVTSITMDRVOHDPAR-BQNGGNYPPRS
Mouse_MannII_[X 1 -----M-----VGSATFCVTSITMDRGHLDYPRGPRQIGSYPPQG
hMannII 1 -----M-----VGSATFCVTSITMDRGHLDYPRNPRREGSYPPQG
CionaMannII_[AR 1 -----M-----LFGGILFFGSIFIGDTPNSPQVRVPSGSEND
ArabMannII 1 -----M-----WPESSYIGHSRSTGGGTGGMGQSLIP-----TALSRLK
Insect_ManIII 1 -----M-----WRTRLCKPSTRLLIFPLAFG-----V
hLyso_MannII 1 -----M-----
hCyto_MannII_[N 1 -----M-----AAAPFLKRWRTTYERERKVSPPYFTDCNLR-----G

Droso_MannII_[X 40 IYENENRREBENGHOEBGEEARNARARTNRD-----
C.elegans_MannI 37 CAMDARRRGMAEVAEENGRTDRBEGEORARAERSVDFDEERKTEEREVEERKEV
rMannII_[XM_218 120 OSVILGMECECLTEEMREESHDSLEANAEGFPALLPY-----
hMannIIx_D55649 46 OSVILGMECECLTEEMREESHDSLEANAEGFPAMLPY-----
Mouse_MannII_[X 47 OSILGMECECLTEEMREESHDSINESVEDGPRGSPG-----
hMannII 47 OSMLGMECECLTEEMREESHDSINESVEDGPRSSQS-----
CionaMannII_[AR 45 CRTILGDRSLERETLEARRERKDSODPMREHVEVPMORGEIR-----
ArabMannII 37 ANRKPRTTIWMPFAMFFALTVSTFFITLPHFGVPGPIS-----
Insect_ManIII 28 YCYFYASPOYHNPRISTPASBHFSSSTHTVK-----
hLyso_MannII 1 -----M-----GYALSGVCAR-----
hCyto_MannII_[N 34 RFGASCPHAVTSSTPTPERLPYQAVORDFRPAQVG-----

Droso_MannII_[X 77 -----DPIRPPLEVARSPRPGCCQDVQDVPHVDOMTEMDRSEFIDID
C.elegans_MannI 97 APVPVRGNRGMABIRQVQRIKPTPSMKDVCGIRENVSIABSDOMIDMDTWPENPD
rMannII_[XM_218 166 -----HTANGSMVLPPEPRSPFSVSPEDCFALGGRGQRPOMITSEDPENNV
hMannIIx_D55649 92 -----YTVNGSMVLPPEPRSPFSISPODCFALGGRGQRPOMITSEDPENNV
Mouse_MannII_[X 93 -----NASQGS-IELHSPOLA-LQADPRDLFASQSGSQPNOMIDMDLPEENPD
hMannII 93 -----NFSQGAGSRLLPSQLS-LSVDTADLFASQSGSENSDOMIDMDLSEENPD
CionaMannII_[AR 94 -----NVMKPVLPPLIMPKQFANDSRMSDTCVLSYGGKSDOMIDMDLPEENPD
ArabMannII 83 -----SRPLTSRSNRIVRPRKINRRPINDSNAGAVVDTTMDLPEENPD
Insect_ManIII 63 -----SDEPTPDQPALKEHADIDTAYPTDQPSMLRT
hLyso_MannII 13 -----GCLDSAGPMTMSRALEPPLPPCFPLLIQAAGAR
hCyto_MannII_[N 71 -----DSFGPTWNTCMFRVELTIPAMGQEVHLCWESDG

Droso_MannII_[X 122 GGVMKQGRIEPLKMAHRKIAVVPVPHSHNDPG-----CT
C.elegans_MannI 157 GGVMKQGRIEAEKVRSLPR-IEVHVPHSHNDPG-----MT
rMannII_[XM_218 219 GGVMKQGRIEISPMIAED-LOVEVVPVPHSHNDPGKEPAGPSRSVQGGLSGDERRT
hMannIIx_D55649 145 GGVMKQGRIEISPMIAED-LOVEVVPVPHSHNDPG-----RT
Mouse_MannII_[X 144 GGVMKQGRIEADHEP-LOVEVVPVPHSHNDPG-----RT
hMannII 145 GGVMKQGRIEISNTEP-LOVEVVPVPHSHNDPG-----RT
CionaMannII_[AR 147 GGVMKQGRIETSDQWAGRK-IEVHVPHSHNDPG-----RT
ArabMannII 132 GGPMKQGRITMDDDIEEK-IEVVPVPHSHNDPG-----RT
Insect_ManIII 101 KEFMDKSEKRIEIRNITTRPR-IEVVPVPHSHNDPG-----RT
hLyso_MannII 48 AGGETCPTOPN-IEVVPVPHSHNDPG-----RT
hCyto_MannII_[N 107 GIVMDGEPGGLTKGKTS-YLTDRLGEDERS-----ITLY

Droso_MannII_[X 162 EERYC-----HDTRETSWARRHHEEMFIWELISFAHHDGEMRLC
C.elegans_MannI 197 EERYC-----ROTRMDGGAELIAKDEMFIWELISFETMRDOADEIKKV
rMannII_[XM_218 277 EERYC-----EOTCRILNSVSRDCEPPRRFHWAEVSFAHHDGEMRLC
hMannIIx_D55649 184 EERYC-----EOTCRILNSVSRDCEPPRRFHWAEVSFAHHDGEMRLC
Mouse_MannII_[X 183 EEDYR-----DTCOYFPMVLEIKDSRRFISEISLSHHDGEMRLC
hMannII 184 EEDYR-----DTCOYFPMVLEIKDSRRFISEISLSHHDGEMRLC
CionaMannII_[AR 186 VERYC-----DTCOYFPMVLEIKDSRRFIWAEVSLSHHDGEMRLC
ArabMannII 171 VEERYC-----ROSRHDTETLSKDSRRFIWAEVSLEHHDGEMRLC
Insect_ManIII 142 EEOYR-----WTKNIEEMWRTBOYFPMVLEIKDSRRFIWAEVSLSHHDGEMRLC
hLyso_MannII 80 VEOYR-----WTKNIEEMWRTBOYFPMVLEIKDSRRFIWAEVSLSHHDGEMRLC
hCyto_MannII_[N 146 VEYACN-----GLLGAGRGSAAPDPTRIFQLSRFAVERDVRMLVDLELLG

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Droso_MannII_[X	214	SLVHNGC	LEIVTGGVWVMPDEAN	RYFA	SLDOLIEG	QRLQF	W	MTFTAS	MAIDPF
C.elegans_MannI	249	GYLHAGC	PEIVTGGVWVMPDEAN	RYFA	SLDOLIEG	QRLQF	W	MTFTAS	MAIDPF
R.MannII_[XM_218	329	RLVHNGC	LEIVTGGVWVMPDEAN	RYFA	SLDOLIEG	QRLQF	W	MTFTAS	MAIDPF
hMannIIa_D55649	236	SLVHNGC	LEIVTGGVWVMPDEAN	RYFA	SLDOLIEG	QRLQF	W	MTFTAS	MAIDPF
Mouse_MannII_[X	235	SLVHNGC	LEIVTGGVWVMPDEAN	RYFA	SLDOLIEG	QRLQF	W	MTFTAS	MAIDPF
hMannII	236	SLVHNGC	LEIVTGGVWVMPDEAN	RYFA	SLDOLIEG	QRLQF	W	MTFTAS	MAIDPF
CionaMannII_[AK	238	TLVHNGC	LEIVTGGVWVMPDEAN	RYFA	SLDOLIEG	QRLQF	W	MTFTAS	MAIDPF
ArabMannII	223	RLVHNGC	LEIVTGGVWVMPDEAN	RYFA	SLDOLIEG	QRLQF	W	MTFTAS	MAIDPF
Insect_MannII	194	RLVHNGC	LEIVTGGVWVMPDEAN	RYFA	SLDOLIEG	QRLQF	W	MTFTAS	MAIDPF
hLyso_MannII	140	SLVHNGC	LEIVTGGVWVMPDEAN	RYFA	SLDOLIEG	QRLQF	W	MTFTAS	MAIDPF
hCyto_MannII_[N	198	IARGLCKDEHRSFQ	TLTANQMVLVCDP	APQ	TFPV	QALASRFFS	QHGGSQRT	TRAT	

Droso_ManII_[X	270	GBSPMPYALICSGFRMILLORTHYSLKRLAQCCLEFP	RCOT	RCMDKGDTA	YTHMMPF
C.elegans_ManII	307	GLSPMPHMLTSAINTHMLQRVHYSRLKALKCLEFP	RCOT	RCSTGEPR	RSBMPF
rManII_[XM_218	375	GBSPMPYALIRANLTSMLLQRVHYAKRFPATRSLEFP	RCOT	RCMSD	STD
hManIIa_D5649	292	GBSPMPYALIRANLTSMLLQRVHYAKRFPATRSLEFP	RCOT	RCMSD	STD
Mouse_ManII_[X	291	GBSPMPYALIRAGFSMLLQRVHYAKRFSLELTLEFP	RCOM	RCWDLG	ATD
hManII	292	GBSPMPYALIRAGFSMLLQRVHYAKRFSLELTLEFP	RCOM	RCWDLG	VTD
CionaManII_[AR	294	GBSPMPYALIRKMKFRMILLQRVHYAKRFLAQCCLEFP	RCOM	RCMSA	STD
ArabManII	279	GBSPMPYALIRMGFRMILLORTHYSLKRLAQCCLEFP	RCOS	RCAMETD	FVBMMPF
Insect_ManIII	250	GBSPMPYALIRAGFSMLLQRVHYAKRFLAQCCLEFP	RCOS	RCAMETD	FVBMMPF
hLyso_ManII	198	GBSPMPYALIRAGFSMLLQRVHYAKRFLAQCCLEFP	RCOS	RCAMETD	FVBMMPF
Cyto_ManII_[N	257	GBSPMPYALIRAGFSMLLQRVHYAKRFLAQCCLEFP	RCOS	RCAMETD	FVBMMPF

Droso_MannII_[X	330	YSYDIPHTCGPDPR	CCQDF	R	GSPLG	CPKVPPT	I	QVAARSD	LDO	LR
C.elegans_MannI	367	YSYDIPHTCGGPEPS	CCQDF	R	PEGGS	CDG	PPOR	I	QVAARAE	LYDOYRR
rMannII_[XM_218	435	YSYDIPHTCGDPRIC	CCQDF	R	PGG	IN	CPKVPPT	RA	QVAADRAA	LLDOYRR
hMannIIa_D55649	352	YSYDIPHTCGPDPRIC	CCQDF	R	PGG	IN	CPKVPPT	RA	QVAADRAA	LLDOYRR
Mouse_MannII_[X	351	YSYDIPHTCGDPRIC	CCQDF	R	PGG	YG	CPKVPPT	EA	QVAVSRAA	LLDOYRR
hMannII	352	YSYDIPHTCGDPRIC	CCQDF	R	PGG	YG	CPKVPPT	EA	QVAVSRAA	LLDOYRR
CionaMannII_[AR	354	YSYDIPHTCGDPRIC	CCQDF	R	PGG	IT	CPKVPPT	VA	QVAVSRAA	LLDOYRR
ArabMannII	339	YSYDIPHTCGP	PAICCCQDF	R	PGF	YEL	CPKVPPT	VE	QVAVSRAA	LLDOYRR
Insect_MannIII	309	DIYSRSTCGGPEPS	ICLSDP	R	PG	---	YSE	TAKKED	QVAVSRAA	LLDOYRR
hlyso_MannII	252	GVNGYNGYNGYNGY	NGYNGYNGYNGY	NGYNGYNGYNGY	NGYNGYNGYNGY	NGYNGYNGYNGY	NGYNGYNGYNGY	NGYNGYNGYNGY	NGYNGYNGYNGY	NGYNGYNGYNGY
Cyto_MannII_[X	313	LYSR	CEPACRGQ	PGVGT	VE	D	NLPSG	HAMVROFLQ	QNGF	QNGF

Dros_MannII_[X	389	SEIATERNVILAPLGDDDFRYQNTENDVCRVYKE	LEFRLNSO-ARFNVQAQFGTLLQYFD
C.elegans_MannI	426	SEIATERNVILAPLGDDDFRIDFENWS	LEFRLNPSK-SEWNVHAQFGTLLSDYFD
MannII_[XM_21B	494	SEIATERNVILAPLGDDDFRQKPCWDQ	QFYVYQVDFVNSK-PRFNVQAQFGTLLS
hMannIIa_D55649	411	SEIATERNVILAPLGDDDFRQKPCWDQ	QFYVYQVDFVNSR-PMLEVQAQFGTLLSDYFD
Mouse_MannII_[X	410	SEIATERNVILAPLGDDDFRSEYTEWD	LCRMVCOOLFSSNSO-PLRNVQAQFGTLLSDYFD
hMannII	411	SEIATERNVILAPLGDDDFRYCYTEWD	LCRMVCOOLFSSNSO-SKFAVQAQFGTLLSDYFD
CionaMannII_[AR	413	SEIATERNVILAPLGDDDFRSLKETND	QDNYAQLISNS-PLRNVQAQFGTLLSDYFD
ArabMannII	399	STIATERNVILAPLGDDDFRISIDEA	AFQRYVQVDFVNSP-PLNARQAQFGTLLSDYFD
Insect_MannIII	366	GSITERNVILAPLGDDDFRYSVE	DAQVYVQVDFVNSHABRIPNAD
hlyso_MannII	303	GRYATERNVILAPLGDDDFRYSVE	DAQVYVQVDFVNSHABRIPNAD
Cyto_MannII_[N	373	YGSAQAPQMECGIRFLTQKLS	LVMSFPBRTFWEGLDGRVLPFPPGDS

[illegible]

Droso_MannII_X	492	DRVLNHYRRAEILSAMHSDW----	MAR-----	IEERVTCARREISLFOBRD	
C.elegans_MannI	529	DRVLQHYRRAEATLTIAMIEE-----	GMVEAR-----	IERVTCARRISLFOBRD	
rMannII_XM_218	601	DRVLEELRRAEVLSTALARRRSGLTGOYPLS	-----D	AVITEARRISLGLFOBRDA	
bMannIIx_D55649	518	DRVLEAELRRAEVLSTAAARRRSLGAGRYPLS	-----D	TLTEARRISLGLFOBRDA	
Mouse_MannII_X	517	DRVLESELRAEVLSTALALCAQRYRINXPLSSP	-----H	TLTEARRISLGLFOBRDA	
hMannII	518	DRVLESELRAEVLSTALALCAQRYRINXPLSSS	-----L	TLTEARRISLGLFOBRDA	
CionaMannII_AR	515	DRVLESELRAEVLSTALMPKIQWTGLGETFSH	-----L	PLVTCARRISLGLFOBRD	
ArabMannII	514	DRVLEELRRAEVLSTALSPFLGYCHRIQCRFPST	-----P	TYTTCARRISLGLFOBRD	
Insect_ManIII	470	ARQPEELRRAEVLSTALVSHYIROMGRGEGFAS	SEKKLERS	ECVTCARRISLGLFOBRDA	
hlyso_MannII	401	DRVSYNPLQVCHOLEAVGLAIVNGPYGSGDSAP	-----	LVETARRISLFOBRDA	
Cyto_MannII_N	474	DRVLR-----	STNTGLDPRQLSSSPROLFSALSDSE	-----	QKTCVGLGFLFELNGT

Droso_MannII_[X	537	ITGTA	TE	VVDY	EO	Q	BA	KACQ	M	Q	S	V	R	T	K	P	S	-	I	Y	S	P	D	F	S	F	S	T	T	D	S	--	R										
C.elegans_MannI	578	ITGTA	TE	VVDY	GO	I	I	D	A	N	A	C	E	D	S	-	T	N	-----	K	-----	C	D	E	R	-	R	-	R	-	R	-	R										
rMannII_[XM_218	655	ITGTA	TE	VVDY	G	V	R	L	S	T	S	T	R	O	I	N	A	B	Y	L	L	G	D	R	E	T	S	P	D	R	A	P	-	C	V	S	Q	A	M	R			
hMannIIa_D55649	572	ITGTA	TE	VVDY	G	V	R	L	S	T	S	T	R	O	I	N	A	B	Y	L	L	G	D	R	E	T	S	P	D	R	A	P	-	C	D	T	-	R					
Mouse_MannII_[X	571	ITGTA	TE	VVDY	G	T	R	L	P	C	S	T	S	T	R	O	G	D	S	A	F	L	L	L	D	R	K	L	Y	O	S	D	S	K	A	-	R	I	N	T	-	Q	
hMannII	572	ITGTA	TE	VVDY	G	T	R	L	P	C	S	T	S	T	R	O	G	N	S	A	F	L	L	G	D	R	L	T	Y	D	S	Y	S	P	D	T	-	E	D	L	K	-	Q
CionaMannII_[AR	569	ITGTA	TE	VVDY	G	T	R	L	P	C	S	T	S	T	R	O	S	Y	S	A	Q	V	I	-----	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
ArabMannII	567	ITGTA	TE	VVDY	G	T	R	L	P	C	S	T	S	T	R	O	S	R	L	E	V	L	G	I	R	R	E	R	S	D	S	P	S	T	E	A	-	C	M	R	S	-	R
Insect_ManIII	530	ITGTA	TE	VVDY	G	T	R	L	P	C	S	T	S	T	R	O	S	R	L	E	V	L	G	I	R	R	E	R	S	D	S	P	S	T	E	A	-	C	M	R	S	-	R
hlyso_MannII	448	ITGTA	TE	VVDY	G	T	R	L	P	C	S	T	S	T	R	O	S	R	L	E	V	L	G	I	R	R	E	R	S	D	S	P	S	T	E	A	-	C	M	R	S	-	R
hCyto_MannII_[N	523	ITGTA	TE	VVDY	G	T	R	L	P	C	S	T	S	T	R	O	S	R	L	E	V	L	G	I	R	R	E	R	S	D	S	P	S	T	E	A	-	C	M	R	S	-	R

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Dros_MannII_X 594 WPGSG EDS-----RTTII GEDILPS EVV AV BN NT PE KE Q VD F Y V S S P F S V T D L A
C.elegans_MannI 628 VNEWL PER-----RVYRIG----- Q N W A S E R T S R N K E P C V D S - L D A G - E A D

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rMannII_XM_218 715 GQST HPSAALVPAALASA LPQR-AP PVV MPL CRRLS V IVNSPR RV SEE
 hMannII_XM_218 630 LSBA P-----ERTV QLDG-SP PVV MPL CRRLS V IVNSPR RV SEE
 Mouse_MannII_X 629 SSQS P-----QRII QLSAQP Y V MPL CRRLS V IVNSATGV SDS
 hMannII 630 SSQS P-----QRII QLSA-EP Y V MPL CRRLS V IVNSPT QV SAS
 CionaMannII_[AR 626 QHQFAP-----VVVR PTNEERAVV QMSH LDRIG V IVNSPD VV SEN
 ArabMannII 627 YDARP HRP-----AAREGNSET V MPS OTREE V VVRAE SV DSN
 Insect_MannII 590 PRK-----QVSPIDRK V MPLAETRE V RSN SN RYDTH
 hLyso_MannII 508 R-----VQV MPLGRVNV V PSEGVV VVDPN
 hCyto_MannII_X 583 -----SCIQVAREA CR ED RSHGT AAAAAALCAGEPGPE

Droso_MannII_X 648 N-NPVEAO SPV V WHDITLTKTIRPOGSTK R IFKAR EP GLATV TIS-DSRPE
 C.elegans_MannI 674 P-PIKRCQ SPVIAYDEKRTLVVNG-----I CFML GP ESVS R VKN-TTTSK
 rMannII_XM_218 774 C-OP SVO SVOM SATMVDP-----V C SVPRV PALGIGVLO QPDLDGPT
 hMannII_XM_218 680 C-OP LAVO SARMS SATRAVPD-----V C SVPRV PALGIGVLO QLGIDGHT
 Mouse_MannII_X 680 C-KPVEVO SAV NDMRTISQA-----A SFLAR PPLGIVR K LESQSSSSH
 hMannII 680 C-KPVEVO SAV DTANTISRT-----A SFLAR PPLGIVR K LESASSNSH
 CionaMannII_[AR 677 K-NVPSQTSPI L DSTEIRTD-----C VELS PA GLAVYR WEDHVDAT
 ArabMannII 676 W-TCVPSQ SPEVCHDDTKLFTG-----EBR Y IA PALGIVR K ANGEVCEK
 Insect_MannII 633 RREHLYO MPSI IQDNCKSIVS-----DTT MFVA PPTTSISYR QERTTSBR
 hLyso_MannII 541 C-RTVPSD VIPP SDQAHP-----GLFA PALCPTSL ACQPRWKPQ
 hCyto_MannII_X 623 C-L IV TLFMRRIRVMALEPRG-----GARSLAV PS CTAPVPPPTSLQPLP

Droso_MannII_X 706 HTSYASHLLLRNPTSLPIGC PED KFGDPR RVGNGLTAPSE---CGLL S QL
 C.elegans_MannI 728 VEITTHNAAEPRSTSPSSSTSGDPT RNDRV AEP GENGM KRATS---LVDD P DL
 rMannII_XM_218 824 LQSSVHYLINGVLSVSRQTT P R DSGTS FA SMRY C MSLG---TGLL S RR
 hMannII_XM_218 730 LPSSVRIYLBGRQLSVSRBA P R DSGTS FA SMRY C MSLG---TGLL S RR
 Mouse_MannII_X 730 LADYVLYND-----GLAENG I BEN VADAGDA RMP A M D-R---TGL ER RT
 hMannII 730 LADYVLYND-----GLAENG I BEN VADAGDA RMP A M D-R---TGL ER RT
 CionaMannII_[AR 727 TRSTVVKP INPRVGFSPKRTSR V D EDCG---F MNDQ VAPSGQ---ECGQS TT
 ArabMannII 727 ATPSKLRYASEPDPFPCPP-----PYSCSKLDNDVTE RMEHCT VEDVR---EGSL R VR
 Insect_MannII 688 CVIPCNH-----CRQYQSNVFO KMMPGC TO ENAV RLVNR---TGFL R YR
 hLyso_MannII 589 ARAPQP-----IPRRSWSPA RMEH RATDPD---TGFL R MN
 hCyto_MannII_X 674 QQ-----PFP VQETDGS R MNGI R KIDPTGRLTSLVLSG

Droso_MannII_X 763 TCSPHVPVPRFLK VRSBGDS---GAYLELPMGPASEVEIGC---V
 C.elegans_MannI 785 NSPFIHYGARKSRK ANGNEDEPA---GAYLELPGDARELRQSS---D
 rMannII_XM_218 881 VEEHQOQVD KLVF RTSED S---GAYLELPGDARELRQSS---PV
 hMannII_XM_218 787 VEEHQOQVD QLVF RTSED S---GAYLELPGDARELRQSS---PC
 Mouse_MannII_X 782 RISRQHEER QFLM TNKRD S---GAYLELPGDARELRQSS---PF
 hMannII 781 RISRQHEER QFLM TNKRD S---GAYLELPGDARELRQSS---PF
 CionaMannII_[AR 782 VEVVKTQEG EVAT TNKRD S---GAYLELPGDARELRQSS---PL
 ArabMannII 781 RSGS-ETVVGEEIGM S P---ES---GAYLELPGDARELRQSS---B
 Insect_MannII 738 RIRKRTVVD QVGAQ---AQRES---GAYLELPGDARELRQSS---H
 hLyso_MannII 628 MHQQLLLPVRQTPFM MASIGDNESDQASAYGERHMQOKPLPVSMAQ---I
 hCyto_MannII_X 714 RALAEAGVGNQFVL DDVPLYWDA---WD MDYH TRRPVIGQAG---T

Droso_MannII_X 808 ILVRSK ESSVSVG---LPS VROT---IMRGS---AP RNLVD G-S-LDNT
 C.elegans_MannI 830 ILVRSK VORVPATPHDLKI OTMT---LYOGL---PM RNEVD R-S-KMP
 rMannII_XM_218 927 RVEEPFPEVAAL YEPHOV RLMN---LPGVEG---LS RSPQVD R-D-YVM
 hMannII_XM_218 833 C---VSLKALSQRMLRT IST T-RR-SG---FT CQGWGRC---T-YVM
 Mouse_MannII_X 828 RVEER YSDVTC LEBVTER RLMN---IQGIEG---QS SNIVE R-N-VN
 hMannII 827 RVEER YSEVTC PDBVTER RLMN---IQGIEG---QS SNIVE R-N-VN
 CionaMannII_[AR 829 RIRCP MSTVBLVPLVLR TLYTGAGTOS---LG R SEDVD R-TGYDM
 ArabMannII 821 VTEESLVQEVF SPRTMERSPLSOKTRLYTGNTLQOV---EYRVE LG-MDFDD
 Insect_MannII 792 IYSGPISTETITM LPPVLT RYVVPDPLSR---A R ETDVPEAPPRRT
 hLyso_MannII 678 RLVTP LCEVRN SAMCSQVRLP---GO---R R RSVSGPIPVGTWC
 hCyto_MannII_X 759 RAVTEGGIRGSAL LLQISPNSRLS QVWLDVGC---Y RPHTEVHREARFLXV

Droso_MannII_X 852 EVVRETR DSGDI---PYTDINGLOPIR---DRLLQAN YP PGM IE
 C.elegans_MannI 879 EVVRETR DSGDI---PYTDINGLOPIR---DRLLQAN YP PGM IE
 rMannII_XM_218 977 EVVRETR DSGDI---PYTDINGLOPIR---DRLLQAN YP PGM IE
 hMannII_XM_218 874 WTSG---TTSTSNWPC---TSIOTSTAR OPIY---DRLLQAN YP PGM IE
 Mouse_MannII_X 878 EVVRETR R ENQHR---PYTDINGLOPIR---DRLLQAN YP PGM IE
 hMannII 877 EVVRETR R ENQHR---PYTDINGLOPIR---DRLLQAN YP PGM IE
 CionaMannII_[AR 882 EVVRETR R ENQHR---PYTDINGLOPIR---DRLLQAN YP PGM IE
 ArabMannII 880 EVVRETR R ENQHR---PYTDINGLOPIR---DRLLQAN YP PGM IE
 Insect_MannII 846 EVVRETR DSGDI---PYTDINGLOPIR---DRLLQAN YP PGM IE
 hLyso_MannII 727 EVVRETR DSGDI---PYTDINGLOPIR---DRLLQAN YP PGM IE
 hCyto_MannII_X 814 EVVRETR DSGDI---PYTDINGLOPIR---DRLLQAN YP PGM IE

Droso_MannII_X 902 DAX---TRITLITACLGSSIASGELE RDRRIASDDERGLGQGVNDKPVLRH R
 C.elegans_MannI 929 DDT---TRITLITACLGSSIASGELE RDRRIASDDERGLGQGVNDKPVLRH R
 rMannII_XM_218 1027 DSO---TRITLITACLGSSIASGELE RDRRIASDDERGLGQGVNDKPVLRH R
 hMannII_XM_218 922 DAX---TRITLITACLGSSIASGELE RDRRIASDDERGLGQGVNDKPVLRH R
 Mouse_MannII_X 928 DAX---TRITLITACLGSSIASGELE RDRRIASDDERGLGQGVNDKPVLRH R
 hMannII 927 DAX---TRITLITACLGSSIASGELE RDRRIASDDERGLGQGVNDKPVLRH R
 CionaMannII_[AR 932 DEX---TRITLITACLGSSIASGELE RDRRIASDDERGLGQGVNDKPVLRH R
 ArabMannII 930 GSG-ORFVH ROSGVASIKK LEMDRRL RDDRGGLGQGVNDKPVLRH R
 Insect_MannII 898 DEX---TRITLITACLGSSIASGELE RDRRIASDDERGLGQGVNDKPVLRH R
 hLyso_MannII 785 DGN---MOLITLDRCCGSSIRDSLE RDRRL RDDRGGLGQGVNDKPVLRH R
 hCyto_MannII_X 858 LSEHGFGHLLNDCKYAS---VRGS LS SLIRAPRAPDATATCR PLYALMPH GSF

Droso_MannII_X 960 EVVHCVRPSKLE-----PAGYL SAARASQSTLDE DKFPAR
 C.elegans_MannI 987 EPMSSSGNRKEE-----RVG RSH GRASSTLDEP KIGDA
 rMannII_XM_218 1085 ERL SPEVOQE-----RSTSPSL SH TSMYLNTPP VPAR
 hMannII_XM_218 980 ERL VGS-EVQDS-----RSTSPSL SH TSMYLNTPP VPAR

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Mouse_MannII_[X 986 E R A NMEERK-----SPVSYPSTLSE TSSFLNRP P V SG
hMannII 985 E R A NTEERK-----S-VSYPSTLSE TSSFLNRP P AN--
CionaMannII_[AR 990 E R A AARESKSS-----AKLAKPSRAVYQSSWEILEP RP S NG
ArabMannII 989 ESNISQADPASNT-----NPRNPSLSE IGARLRYE NTFIAXK
Insect_ManIII 956 ESMCPG TRAKRDTSEPGFPVWERRRFGPGQKESPYQVPSOTADYISRMFMYE NVYI DT
hLyso_MannII 843 VLLDTAQAAAAGHR-----LAEQELAEQ V LAPGG
hCyto_MannII_[N 916 QDAGV CAAYSLN-----EHLALPAPSAPATSM SAFS SS

Droso_MannII_[X 1000 NEWIGAGGQ-----FGGDEFSAREDD SV RRLTKS-----
C.elegans_MannI 1027 TPESISSXN-----EQRPFCD BL TPR ASPTTY-----
rMannII_[XM_218 1126 RESTSPT E---SEPTIASPLPCDFELLMLRM PAEVSVVVRANPHERQAEPCLLGRRAAD
hMannIIx_D55649 1020 MQLPGPG R---SEPTIASPLPCDFELLMLR QAE-----
Mouse_MannII_[X 1027 -QLPSPAYELLSEFPILQSSLPCH BL MLR QSKMG-----
hMannII 1023 -KPSPT ELQGEFSPLOSSLPCCH BL MLR QSKVG-----
CionaMannII_[AR 1032 -----P ELKED RSIPOLPCCH BL MLRA ESKDA-----
ArabMannII 1029 PDISVR PQYGSFAPLAKPLPCCH BL MF VPRPSKYS-----
Insect_ManIII 1016 SEVGEIE KP---OSFLOSFPFG BL TLR TDDVLE-----
hLyso_MannII 875 GAAYNLGAPPRTQPSGPRRDLEPS BLITLA WGPBMVLR-----
hCyto_MannII_[N 953 PAVVLET R---QAESFPQRRLSVLRLEYAR-----

Droso_MannII_[X 1032 -----SARTQRY Y ERTFLMCC TPEERTQKLDVCHLLPFWARCERTT TFL
C.elegans_MannI 1059 -----EAMERST EERKAAMVMERV PDCR-SRLTLPTDSCLATGLEIEP I I
rMannII_[XM_218 1183 PPPLLSLTVPQDTLPAAD ERLEREG DC EARN GPNC T OGRLAIGSLPHG D L
hMannIIx_D55649 1054 -----DTLP AETAL ERLEREG DC EARN GPNC T OGRVAIGSLPHG D V
Mouse_MannII_[X 1064 -----KGY DE EAL ERLEREG DC OFSS G GLPC T OGRMSVLKLPNKA E
hMannII 1060 -----NGE NE EAL ERLEREG DC RFSS GTGLFC T OGRILVQKLLNKFIE
CionaMannII_[AR 1064 -----VAP DQS EAL ETVGRCS DADRYEPTCLMEGVERIAITIST PTH
ArabMannII 1068 -----QLEEDKPRPA ERLEREG DC EARN GPNC T OGRVAIGSLPHG D V
Insect_ManIII 1052 -----LPP NESY ERLEREG DC EARN GPNC T OGRVAIGSLPHG D V
hLyso_MannII 916 -----LEHOF AVE ERLEREG DC EARN GPNC T OGRVAIGSLPHG D V
hCyto_MannII_[N 981 -----G RVDC ERLEREG DC EARN GPNC T OGRVAIGSLPHG D V

Droso_MannII_[X 1081 QMPEHLDGM APEVCPME-----TAAY SESS-----
C.elegans_MannI 1107 STPSAKRS TNLYEGN-----KAEQRIQEM IS I SP-----
rMannII_[XM_218 1243 F-HOP STPS YPLASPS-----ESTD YLEPMEIST EUG-----
hMannIIx_D55649 1103 F-HOP STPS YPLASPS-----ESTD YLEPMEIST EUG-----
Mouse_MannII_[X 1112 S-HVP STPS RSPPDAQ-----NMSE YLEPMEIST EUG-----
hMannII 1108 S-HTP STPS RSPPGTO-----NISE YLEPMEIST EUG-----
CionaMannII_[AR 1112 SG RR STPS EHDGSLLD-----NOGG YLEPMEIOA VIT-----
ArabMannII 1119 SR RP STPS QEDMEILGYDQELPRDSSQPREGR YLEPMEIOA VIT-----
Insect_ManIII 1100 SLTGLR STPS TG-----LSD ELMANES RT EUG-----
hLyso_MannII 965 SRPRW EHT GPTPHQTPY-----QLDPAN YLEPMEIST LAS QWKEVDG
hCyto_MannII_[N 1027 SAPVARA LASATLSPWG-----WGFVCRDWG ILSASPA-----

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Citation

Algorithm Citation:

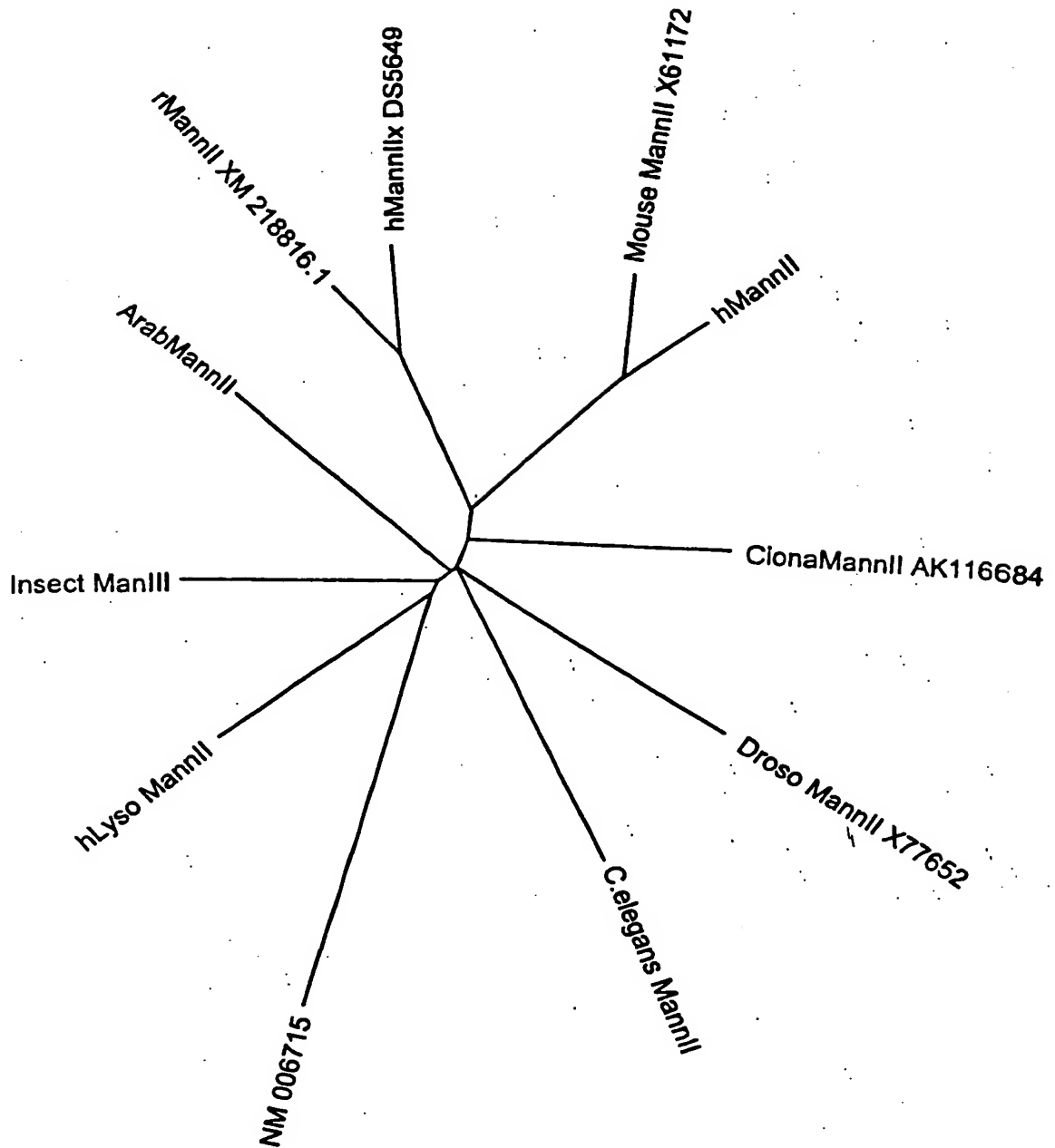
Not given, but presumably Kay Hofmann and Michael D. Baron.

Program Citation:

Boxshade version 3.3.1, by Kay Hofmann and Michael D. Baron.



FIG. 24



Arabidopsis thaliana Mannosidase II (NM_121499)

1 ATGCCGTTCTCCTCGTATATCGGCAACAGCCGCCGTAGCTCCACCGCGGAGGAACCCGCGGTTGGGCGCAATCTCTTCTTCCAACAGCGTTATCAAAGTCAAACTAG
1 MPFSSSYI GNSRSTT TGGGTGGGWGWSLLPTALSKSL
110 CGATCAATCGAAACACGAAACGAACCTCTCGTAGTCAATTTTCATCTCGGCAACTCTCTGTGATCGCACTCAGCGCTCAGCTCTCTTCTCTCTCTCATCTCTCT
37A I N R K R K R T L V N F I A N F V I A L T V S L L F F L L L T L F
219 CCATCTCGGGGTACGAGCGAGTCTCTCAGGATCTCTACCTCAGATCCAATCGGATCGTCAAGCCAGGAAGATTAATCGCCGACCTTAAACGATTCCAAT
73 H F G V P G P I S S R F L T S R S N R I V K P R K N I N R R P L N O B N
328 TCAGCGCCCGTGTGATATCAACAATCAAGATCTATACGATAGGATGAGTTTCTTGATACAGATGGTGGTCCATGGAACCAAGTTCGAGAGTTACGATTAAGACG
110 S G A V V D I T T K D L Y D R I E F L D T D G G P W K G W R V T Y K D
437 ATGAGTGGGAGAACGAGAGACTCAAAATCTCGGTTCCTCATCTCATACGATCTCGGTGGAAATGACTGTAGAGGAGTATTACAGACAGAACTCCAGACATAT
146 D E W E K E K L I F V P H S H N D P G W K L T V E E Y Q R O S R H I
546 TCTTGACACCACTGTTGAGACTTTATCTAAGGATTCAAGAAGAAAGTTTATATGGGAGAGATCATATCTGGAGAGATGGTGGGAGAGCGCTTCACTTAATAAACA
182 L D T I V E T L S K D S R R K I W E E M S Y L E R W R D A S P N K Q
655 GAAGCTTTGACTAAATGGTGAAGGATGGGAGCTAGAGATTGTTGGAGTGGTGGGTTATGAATGATGAGGCTAATTCACATTATTTGCCATAATTGAACAGATAG
219 E A L T K L V K D G L E I V V G G W M N D E A N S H Y F A I E Q I
764 CAGAGGGTAATATGTGGCTCAATGACACAAATGGGGTTATCTGAAGAATCTTGGGCTATAGATCCCTTGGCTATCATCAACCATGGCTATCTCTCGGGGTAT
255 A E G N M W L N D T I G V I P K N S W A I D P F G Y S S T M A Y L L R R M
873 GGGTGTGAAAACGCTTATTCAAAGGACTCATTACGAGCTCAAGAAGACCTTGGCCAGCATGAAGATTTGGCGTCAAGCTGGGATCTGGAA
291 G F E N M L I Q R T H Y E L K K D L A Q H K N L E Y I W R Q S W D A M E
982 ACCACAGATATCTTTGTTTCATATGATCGGCTTTTATTTCATACGATATCCCAACACTTGTGACAGAGCTGCAATTTGCTGTAGTTTGATTTCGCTCGGATCGGG
328 T T D I F V H M M P F Y S D I P H T C G P E A I C C O F D F A R M R
1091 GATTTAAGTATGAATCTGTCCATGGGGAAGCAGGCTGGAGACCACTATGAAGATCTGACGAGGAGGCAATTAAGCTTCTGGATCAATACAGGAAAAATCCAC
364 G F K Y E L C P W K K H P V E T T L E N V Q E R A L K L L D Q Y R K K S T
1200 TCTATATCGAACTAATACACTTCTTATACCTCTTGGAGATGATTTTAGGTACATTAGTATCGATGAAGCCGAGGCTCAGTTTCGTAACCTACAGAGATGTTGTTTATC
400 L Y R T N T L L I P L G D D F R Y I S I D E A E A Q F R N Y Q M L F D H
1309 ATCAACTCTAATCTAGTCTTAACCGAGAAGCAAGTTTGGTACTTTCGAGGATTAATTCAGAACAGTCCGAGAAGAAGCAGACAGAGTGAATTAATCTCGTCTGGT
437 I N S N P S L N A E A K F G T L E D Y G F R T V R E A D R V N Y S R P G
1418 AGGTTGGCTCTGGTTCAGGTTGTGGTTTCTCTCTCTGCTGAGTACTTCTTACATGACGATAGGCAACAGACTTGGAGTGGTATTATGTTTCAAGAGCTTT
473 E V G S G G Q V V G F P S L S G D F F T Y A D R Q Q D Y W S G Y Y V S R P F
1527 CTCAAAGCTGTGTGATCGTGTGCTCGAGCATACCTTCTCGGAGCTGAGATCATGATCTCATTCTGCTAGGTTATGGCATCGAATTCATGTCGAGAAATTTCCAAC
509 F K A V D R V L E H T L R G A E I M M S F L L G Y C H R I Q C E K F P T
1636 AGTTTTCAGTAAAGTGTACTGTCTCAAGAAGAAATCTGGCTCTTTCCAGCAGCATGATGGGTAATCGAATCTGTAAGGATTAATGTGGTACAAGATACCGGCAACC
546 S F T Y K L T A A R R N L A L F Q H H D G V T G T A K D Y V O D Y G T
1745 GGATGCATACTTTCATTGCAAGAGCTTCAGATCTTATGCTTAAAGCAATCGAAGTTCTTCTGGGATCGCCGACGAGAAGAAAAATGATCAATCCCATCACTTTT
582 R M H T S L G Q D L O I F M S K A I E V L L G I R H E K E K S D Q S P S F F
1854 CAGGCGAGAGCAATGAGATCAAAGTATGATGCTCGGCCAGTTCACAAGCCAATTGTCTGCCCGGAAGGAAATTCGCACACAGTTATACTCTTCAATCCATCAGAACAG
618 E A E Q M R S K Y D A R P V H K P I A A R E G N S H T V I L F N P S E Q
1963 ACAGACAGAGGAGTGGTGAAGTTGTTGTTAAACCGCTCAAAATCTCGGTTTGGACTTGGACTCAAACTGTGCTCTAGCCAAATTTCTCTGAAGTGCAGCATGACG
655 T R E E V T V V V N R A E I S V L D S N W T C V P S Q I S P E V O H D
2072 ATACCAACTATTACCGGAGACATCGCTTTACTGGAAAGCTTCCATCCAGCTCTTGGTCTGAGAACATTTTCAATGCTAATGGGAATGTCGAGTGTGAGAAAGC
691 D T K T G L T G R H R L Y W K A S I B A L G L R T Y F I A N G N V E C E K A
2181 TACTCGCTTAACTCAAAATCGCTTCTGAGTTTGACCCATTTCTCTCTCCATATTCTGCTCCAAATCGACAACGAGTCTAGATCGAAATGAACAT
727 T P S K L K Y A S E F D P F P C P P P Y S C S K L N D V T E I R N E H
2290 CAGACTCTTGTGTTGATGTGAAGAAGCGGATCCTCGGAAGATAGCTCCATAGAAACGGATCAGACAGTCTGTGGGAGGAAGATAGGTATGTACTCTAGTCCAGAGA
764 Q T L V F D V T W K N S G L R K I V H R N G S E T V V G E I G M Y S S P E
2399 GTGGAGCTTACTGTTCAAAACAGATGGTGAAGCTCAGCCAAATGTTCAACTCAGATGACGATGATGACTCACTCTCAGGGGTCTCGCTGTTCAAGAACTCTCTCTACCC
800 S G A Y L F K P D G E A Q P I V Q P D G H V U T S E G L L V Q E V F S Y P
2508 TAAACCAAAATGGGAGAAATCACCCCTCTCTCAGAAAACTCGTCTTACACTGGAGGTAAATACGCTTCAGGATCAAGTGGTGCAGATAGAATATCATGTTGAGCTTCTT
836 K T K W E K S P L S Q K T R L Y T G G N T L D Q V E I E Y H V E L L
2617 GGTAATGATTTGATGACGGGAATGTGTCGGGTACAAGACTGATGTTGACAAAGCAAGGCTCTTCTATCAGATCTCAATGGTTTCAAAATGACGAGCAGAGAAA
873 G N D F D D R E L I V R Y K A T D V D N K K V F Y S D L N F G Q M S R R E
2726 CTTATGATAAGATCCCTCTCAAGGAACACTACCAATGCCATCTCTCGCATTTACCAAGGATCCAATGGTCAGAGATTTCCGTCGATCTCTGCTAATCTCTCGG
909 T Y D K I P L Q G N Y P M P S L A F I O G S N G O R F S V H S R O S L G
2835 TGTTCGAAGCTCAAGAGGGGTTGGTGGAGATTATGCTGGACAGACGGTGGTTCGTGATGACGGAGCGGGTCTAGGGCAAGGCTGATGGATAACCGGCAATGACC
945 V A S L K E G W L E I M L D R L R V R D D G R G L G O G V M D N R A M T
2944 GTGGTATTTCACTTCTCTCGGAATCTAACAATTTCTCAAGCAGACCTGTCTCAACCACTAAACCCGGAAGAACCTCTCGCTCTCTCTCACTCTAGGTGCTCACTTAA
982 V V F H L L A E S N I S Q A D P A S N T N P R N P S L L S H L I G A H L
3093 ACTACCCCAATAAACACATTTCATGCGCAAGAACCGCAAGACATATCTGTGGGTGCTCCACATACGGTTCTCTTGTCTTACGCAAAACCGGTACCATGTGACCTCA
1038 N Y P I N T F I A K K P Q D I S V R P O Y G S F A P L A K P L P C D L H
3162 CATTGTAATTTCAAGGTTCTCTGTCATCAAAATCTCTCAGCAATTTGGAAGAAGCAAGCCAAAGTTTCGCTCTTATCTCTCAATAGACGAGGATTTGGGATTCACTTAT
1054 I V N F K V P R P S K Y S Q L L E E D K P R F A L I L N R A W D S A Y
3271 TGGCATAAAGGAAGCAAGTAACTGCACAGACTGGCTAATGAACAGTAACTTTCCGACATGTCFAAGATCTTGAGCTCTCAAGGTAACCACTCACTGTA
1091 C H K G R O V N C T S M A N E P V N F S D M F K D L A A S K V K P T S L
3380 ATCTCTTGAAGAAGATATCGGAGTTCTTGGGTACGATGACCAAGAGCTACCTCGAGATAGTTCACAGCCACGGGAAGAGCTGTCTCGATCTCTCCATGGAAATACG
1127 N L L Q E D M E I L G Y D D Q E L P R D S S O A C P R E G R V S I S P M E I R
3489 AGCTTAAGCTTGAACCTGCGACCTCACAAGTGA
1163 A Y K L E L R P H K

C. elegans Mannosidase II (NM_073594)

1 ATGGGAAAACGCAAACTTCTATATTCTCTATGTTGGGAGCTCTTCTCACCGTATCACTCTATTGTGACAAATGGAATGAAACCGGAGCTGAAGCGCTCACCACAAACGACA
1 MGKRNFIILCLGLVATLVSLYLYNGIETGAEALTKRQ
11 AGCAAAATGATTACCGCGGAAAAATCGGAAATTTGGAGCTGTAGCAGAAAGAAATGGAAGAACGATAGACCGTTGGAAACAGAAAGTTCAACGAGCAAAAGCTGAAAAAT
17 ANDLRKIGNLEHVAEENGRTIDRLEQEVQRAKAEK
21 CGGTGATTTTGTATGAAGAAAAGAAAAACGGGAAGAAAAGAACTAGAAAAGAGGAAAAAGAGTTGCACAGTTCCAGTTTCGAGGAAATCGTGGTGAATGGCTCAT
74 SVD FDEEKEKEEVEKEEKEVAPVPVRGNRGEAMH
31 ATTCATCAAGTAAGAACCATATCAAGCCAACTCCATCGATGAAGATGTTTGGAAATAGAGAAAACGTCAGCATGCTCATTACAGCTCGAGATGCTCGATCTCTA
111 IHQVKHQHIKPTPSMMDKDVCGGIRENVSIASHDLQMLDLV
441 TGACACCTGGAAGTTGAAAAATCCAGACGGAGGTGTATGGAACAAAGATGGAAATTAATACGATGCAGAGAAAGTCAAACTCTCTCCACGTTTGGAAAGTTATGTGA
147 D T W K F E N P D G G V W K Q G W K I E Y D A E K V K S L P R L E V I V
551 TACCTCATCTCATTGTGATCCCGGATGGATTATGACTTTGCAAGAGTATTACAACAGACAACTCGCAATATTCTTGATGGAATGGCTAAACATTGGCAGAAAAAGAC
184 I P H S H C D P G A W I M T F E E Y Y N R Q T R N I L D G M A K H L A E
661 GAAATCGGGTTATATGCAAGAAATCATTTTTCGAAATTTGGTGAGAGACCGGAGCATGAAATTAAGGAAAGGTTAAAGGATATTTGGAAGCAGGAAAGTTTGA
221 E M R F I Y A E I S F F E T W R D Q A D E I K K V K G Y L E A G K F E
771 AATTTGTTACTGGCGGATGGGTTATGACAGATGAAGCTAATGCACATTATCACTCAATGACTCAATTTGTTGAGGACATGAATGGATTCAAAATCTTTGGGAAAAA
257 I V T G W V M T D E A N A H Y H S M I T E L A C T F A C T C T G C T A A T A T A A C C A A T G C T G T A A T T C A A A G G T C A T
881 CGCGCATCCCAATCTCATTGGTCAATGTCACTCGGTTTATCACCATCAATGCCCATCTCTAECTCTGCTAATATAACCAATGGCTGTAATTCAAAGGTTCAAT
294 S A I P Q S H W S I D P F G L S P S M P H L L T S A N I T N A V I Q R V H
991 TATTGGTGAACGCTGAGCTGTCTGAAAAAAGATCTGAATTTACTGGAGCAAAATTTATGGATCAACTGGACATCTGATCTCGTTCACATATTATGCTTCTTA
331 Y S V K R L E A L K K N L E F Y W R L F G S T G H P O L R S H I M P F Y
101 CTCTTACGATATACCTCATACGTTGGCCGAGAACCGTCTGTTTGTCTCAATTCGATTTCCGTAGAATGCCAGAGGTTGGAATCATGTGATGGGAAATCCCTCCAC
367 S Y D I P H T C G P E P S V C C Q F D F R M P E G G K S C D W G I P P
1211 AGAAAAATACGATGCAATGTGGCTCCAGAGCTGAAATGATTTATGATCAATATAGAAAGAAAGTCAACTTTTCAAGAATATGTGATTTTCAACCACTTGGAGAT
404 Q K I N D N N V A H R A E M I Y D Q Y R K S Q L F K N H V I F Q P L G D
1321 GATTTGAGTACGACATGATTTTGAATGGAATTCACAAATATAAAATATGGAATTTGGAATACATGAATTCAAATCAGAATGGAATGTTTATGCTCAATTCGG
441 D F R Y D I D F E W N S Q Y E N Y K K L F E Y M N S K S E W N V H A Q F G
1431 AACTCTTTCTGATTTTCAAGAAGCTTGATACTGCAATTTCTGCGCTCGGCGAGCAACTTCAAACTTTTTCGGAGATTTCTCACTTATCGGACAGAGATGATCAT
477 T L S D Y F K K L D T A I S A S G E Q L P T F S G D F F T Y A D R O O H
1541 ATGGATGGATACCTCACTTCGCTCCGTCATTTCTATAACAGCTTGATCGGGTTTCCAACTATTATTAAGATCAGCTGAAATCGCTTACCTTGCAAATATTGAAGAA
514 Y W S G Y F T S R P F Y K Q L D R V L Q N Y L R S A E I A F T L A N I E
1651 GAAGGAATGGTGAAGCGAAAAATTTTGAGAAGCTTTGTGACTCTCAGCAGGAGCTTTCTCACTTTTCCAACTACAGATGGTGTAACTGGTACCGGCAAAAGATCAGCTCGT
551 E G M V E A K I F E K L V T A R R A L S L F Q H H D G V T G T G T A K D H V V
1761 CTGGATTTATGGTCAGAAAAATGATTGATGCTTTGAACCGATGTGAGGATATTCTTTGGGAAGCTCTGTTGATTTGCTGGGAATGATTAACGAATAAAGATCGAGATGG
587 L D Y G Q K M I D A L N A C E D I L S E A L V L L G I D S T N K M Q M
1871 ATGACGATAGAGTTAATGAAACCTTACCCGAAAAAGCTGCTATAAAATGGGCAAAAGCTCGTATTGTTCAATACITTTATCTAGAAATCGCAACGAGCCAAATTTGT
624 D E H R V N E N L L P E K R V Y K I G Q N V L F N T L S R N R N E P I C
1981 ATTCAGTTGATTTCTTGACGCTGGTGTGCAAGCTGATCTCCAATTAAGAAACAAACAACTTTCCGCGGTTATGTCATATGATGAAGAGAAAGAAAGCTGTTGTCAA
661 I Q V D S L D A G V E A D P P I K K Q Q V S P V I A Y D E E K K T L V V K
2091 AAAACCGAATATTGCAACTTTGCTTCATGTTATCACTTGGACCAATGGAGTCTGTCAGTTTCAGACTGTGAAAAATACAAACAACTCAAAAGTGAAATATCACCAATA
697 N G I F E L C F M L S L G P M E S V S F R L V K N T T T S K V E I I T N
2201 ATGCGGAGCAATTCAGAAAGAAACAAAGTTTAAATCTTATCACTCACTCTCGGAGACTTTACTGTGAAAAACGACAAAGTTGAAGCTGAATTTGATGGAGAAATGGAATGATT
714 N A A E F K E T S F K S S T S G D F T V K N D K V E A E F D G E N G M I
2311 AAAAGAGCTACCACTTGTGTTGATGATTAACCAATGATTGGAATTTCACTTATTATCATTTGGAGACCGGAAGTCAAGAGAAAGTTCCGAATGGAAATGAAGACAA
772 K R A T S L V D D K P I D L N S F I H Y G A R K S K R F A N G N E D N
2421 CCGCGCTGGCGCATACCTGTTCTCTCCGATGGAGAAGCTAGAGAACTAAAAACAAATCAAGTGAATGGATTTGGTAAAGAGAGAAATGTTTCAAAAGGTTTTCGAA
807 P A G A Y L F L P D G E A R L K Q S S D W I L V K G E V O K V F A
2531 CTCGAAAAATGATCTGAAATATTPGAAACGCTACACACTTATCAAGGGCTTCCATGGATTGATTGGATATGAAGTTGATGTAGCTTCAAGGAGAAATTCGAGTTG
844 T P N N D L K I L O T Y T G T Y L Q G L P W I D L N E A V D R S K N E F L
2641 GCATCAGATTCACTTCTCAGTAATAGTGGTATGAGTTTTCACATGATCAATGGAATGCAATGATAAAAAGGAGACGACAACTAAATACCAACACAGGCCAA
881 A L R F S S S V S S G D E F F T D L N G M Q M I K R R R Q T K L P T Q A N
2751 TTTCTATCCCATGCTGCTGGTCTTACATTGAAGACGATACTACCAAGATGTCAATCTCGGACAGGCTCTCGAGATTAGCATCTCTCTCGGAGCAAAATGAAA
917 F Y P M S A G V Y I E D D T T R M S I H S A Q A L G V S S L S S G Q I E
2861 TAACTGTTGATCGACCACTAGTTTCAGATGACAAACAGAGCTTTCAGCAAGGAGTTAGACAAACAAACGAACTGGACATTTCCGATTTGTTATGAGGCGATGCT
954 I M L D R L S S D D N R G L O G G V R D N K R T V A H F R I V I E P M S
2971 TCATCGAGTGGTAAATGAAGGAAGAAGACAGATGTTGATTCATTCATGATGTTGATCTGCTGATGCTGCTCTCTTCAATTTCTCTCAAAATGATTGGAGATGCAAC
991 S S S G N K K E A R V G F H S H V G H L A T W S L H Y P L V K M I G D A T
1081 ACCAAAAATCTATTTCCTCGAAAAATGTGGAACAGAGCTGAACCTGACCTGCATCTAGTGACATTTAGAACCACTGGCAGCTCGGCGCAACCTACGAAGCCCAACAGGAAT
1027 P K S I S S K N V E Q E L N C D L H V F R T L A S P T T Y E A N E R
1191 CTCAGCGAGCTGAGAAGAACGAGCGATGGTGAATGATGATAGAGTTGTTCCAGACTGTAGATCCAGGCTTACCTCCGACAGAGCTCATGCTTAGCTACTGGATTGAAT
1064 S T A A E K K A A M V M H R V P D C R S R L T L P D T S C L A T G L E I
3301 GAGCCACTAAATGATCTGACACTGAGCTCGGAAAAAGCTCACTAACCAATTTTATGAAGGAAACAGGCTGAACAAATTCGACTCCAACCAACGATATTTTC
1101 E P L K L I S T L K S A K K T S L T N L Y E G N K A E Q F R L Q P N D I S
3411 CAGTATTCTGTATCATTTTAA
1137 S I L V S F

FIG. 27

Ciona intestinalis mannosidase II (AK116684)

1 ATGAAGCTCAAAAGCCAGTCTTATTTCTTTGGTGGAAATCTGTTCTTCGGAGATATCTGGTTATGATAGGCTCAACTTGACACTCTTAATTCGCCACAGAAAGTCAAA
10 M K L K R Q F L F F G G I F F G S I W F M I G Q L D T P N S P Q K V K
110 TCTCGGAAGCGAGTAAATGACCAATTCGAACTCTCAAGCAAACTTAGTCTGGTGGAAGAAATGTTGTAAGAAATCGTAAATATGCAACAGGTGAAAGATAG
37 F F G S E N D O V R T L O D K L S L V E K E L L E N R K I M H K V K D S
219 TCTACAGGATGACACCCATGAAAAATGTTTCATGCGCTATGCGAGCGGGAGAAATGAAGAAACAGCTCAATAAACTGTGCTACCACTATAATGCCCAAGCAATT
73 L O D M T P M K N V H V P M Q R G E I R N H V N K P V L P L I M P K Q F
328 GCGAATGACTCCGGAATGAGTACACGTGTCCTGTCTCTGCTACCGTGCGCAAGTCCGATGTTAACTGATTAACGTGTATGATCATCTCCATTGTGATGATCCAG
110 A N D S R M S D T C P V L T S Y S G G K S D V N M I N V Y D H L P F D P D
437 ATGGTGGAGTTTGGAACAAGGTTGGGACATCGAGACATCGGATCAGGATGGGCTGGGAGAAATGAAAGTGTTCATTGTCCCTACCTACATATGATCTCGTTG
146 D G G V W K Q G W D I Q T S D Q E W A G R K L K V F I V P H S H N D P G W
546 GTTAAAGACCGTGGAAGATACCTTCAGCGATCAAAACACATATTCTCAATAATATTGTCGATGCTTTGAGTCAAGACCTGCAAGGAAGTTTATCTGGGACAGATG
182 L K T V E R Y F S D Q T Q H I L N N I V D A L S Q D P A R K F I W A E M
655 TCGTATCTCTCAATGTGGTGGGACATTCGCCACCTGATCGTAAGCAGAAATGCAGACACTCGTGAAGATGGACAGCTTGAGATAGTTACGGGTGGTGGGTGATGA
219 S Y L S M W W D I A T P D R K Q K M Q T L V K N G Q L E I V T G G W V M
764 ATGATGAAGCAAACTCATTACTTGTCTATGATGATCAACTCATGAAGTATGGAATGGTTGAGGCGCAACTGAATGTTGTTTCAAAAGTGGGTGGGCGATTGA
255 N D E A N T H Y F A M I D Q L I E M E W L R R T L N V P V K S G W A I D
873 TCCCTTTGGTCAACCCCTCAGCTGGCTTATATGATGAACAGATGAAGTTCAAAAACACTGCTGATACAAAGAGTCCATTATGCACTGAAGAGATCTTGCTCAGGAA
291 P F G M T P T M A Y I L K Q M K F K N M L I Q R V H Y A V K K Y L A Q E
982 AAGTCTCTGGAATTCAGATGGAGACAAATGTGGGATTCAGCTTCAAGTACAGACATGATGTCATCTCATGCTTCTTATTATATGATGTTTCTCCTACTGTTGGCC
328 K S L E F R W R Q M W D S A S S T D M M C H L M P F Y S Y D P V P H T C G
1091 KAGACCCCAAGATTGCTGCCAGTTTCATTGCTGCTTACC CGGCGGCAAGATAACTGCCACTGGAAAGTTCTCTGTTGCCATCACTGACTCCAATGTAGAAAC
364 P D P K I C Q Q F D F A R L P G K I T C P W K V P P V A I T D S N V E T
1200 ACGAGCGCGGAATACTACTTGACCAATATAGAAAAAGTCAAAACTCTTCAAAAGTGACACCTGCTTATTATATTAGGAGATGATTTCGTTATTGCTGAGGCAAGGA
400 R A G I L L D Q Y R K K S K L F S S D T L L I L G D D F R Y S L S K E
1309 ACCAAGTACAGTTTGACAATACGCTCGAATTTCTGATGTGAATTCGCCACGAGTTTAAACGCAAAATCTCAGTTTGGAACTATTCCGAATATTTTGATGCCA
437 T N D Q F D N Y A R I S Y V N S H P E L N A K L O F G T L S E Y F D A
1418 TGAATCTGAAGTGGGGGAGAGGAAAACTCCAGCTTTAAGTGGTGATTTCTTCACTTATGCTGATAGAGAAGATCACTATGGAGTGGTTACTACTCTCAGCGGC
473 M K S E V G G E E K L P A L S G D F F T Y A D R E D H Y W S G Y Y T S R P
1527 TACCACAAAATCGAGGACAGAGCTCTGGAAAGCCACTCTCGAGGAGCAGAAATGTGTTTGGCGCTCATGCGCCCAAAATCCAGTGGACAGGACTTGGTCAAACTTT
509 Y H K M Q E R V L E S H L R G A E M L F A L S W P K I Q W T G L G E T F
1636 TCACATGAACCTTAACTCAGTGGTGGTCAAGCAGCTCAAAATCTTGGTTGTTTCAACACACAGATGGTATAACAGGCGACAGCAAAAGGATCATGTTGTTGTTGATTAGC
546 S H E L Y P L L V Q A R O N L G L F Q H D G I T G T A K A D H V V V D Y
1745 GGAATAAACTCATGAAGAGTGTATGGATGCAAGAAGGTAAATTCATACAGTGCCCAAGTTCTGTTGCAAGAAGATGATCAGGTTGATCCAAATACCATGGTACTTAA
582 G N K L M K S V M D A K K V I S Y S A Q V L L Q E M I T F D P N T M V L
1854 CTATGATGAGGTGTATCAAGCTCAGAACCAACAACTCGCCCTGTGGTTGTTAAGCTACCAACGAAGAATGAAGAAGCGCGGAAAGTCGTTCTCTACAACCTCTCGGAT
618 Y D E V A Q Q N Q O P A P V V W K L P T K N E E A R K V L Y N S L D
1963 TACGACGAATCGGTGTGCTGCTTAATTTGTTACGTCAACCGAGCTGGTTGTGATGTCAGAAAAACAAAGCTCGTTCCATCGCAAAACAGTCCGATCTGGTCAGATT
655 Y D R T G V V R L I V T S P D V V M S E N K N V V P S Q T S P I W S D
2072 CGACCGGAGATCCGACAGACAGTGTGAACCTGTTTTCTTTCAACTGTTCGGCGATAGGACTGGCGGTGTACAAGATATGGGAAGACAACGAGCTAGGACAGACAC
691 S T E I R T D Q F E L V F L S T V P A I G L A V Y K I W E D N D V A O T T
2181 GCACCTCAACTGTTAAGTTTATCAACCCGAGAGTTGGGTTTTCGAAACGAACCCGAGTAAGTTGTACTCGACGTTGAGGATAGCGGGGAGTTTACCATCATGAATGAC
727 H S T V K F I N P R V G F S K R T R S K F V L D V E D S G E F T I M N D
2290 CAATTAGTTGGCGATTCTCTGGACAAAGCGGATGCTCGAGTCACTGACCTAGCTGGGTGACAAAGTCAAAACGCAAGCTCGGAATGTAATTCGTGCTTATATCTCTC
764 Q L V A H F S G O N G M L Q S V T T V R D N V K T Q L G I E F A V Y T S
2399 GTAATAAGAAAGACAAGAGCGGCGCTTACTTGTCTGCTGCTGGACGAGCAACCGCATGTAAACAGAACTCCACCGACCGGTAGTAAGGATCATCAGGCGGTCAGT
800 R N K K D K S G A Y L F L P A G P A Q P H V T E S H R L V R I R G P V
2508 GATGTCAACGGTGCATGTTCTACTACCGAAGCTTCTGCATAAGTACCCTATACACCGGTACTGGTGCAGGCGACCGAGTCTTAGCGGTCCACGCTCTCAACGACGTC
836 M S T V H V L L P N V L H K V L T Y T G T G A G T Q S L V G H V S N D V
2617 GACGTTAGAATGGGTACGACAAACAAAGCTCAGTATGAGGTAAACAGCGAAGTTTATCGGGAAGCAATCTTACGGAATTTAAACGGTTTCAAAATCAACCCC
873 D V R T G Y D N K L S M R L N S E V L S G S K F T D L N G F O I Q P
2726 GAACCCGATTTCAAACTGCCACTACAAGCAAACTCTACCCCAATACCCCAATGGCGTTTATCAAGACGAAAAATCAAGATTAACTTGATGACGGGCGCAACCT
909 R T T Y S K L P L Q A N F Y I P T M A F I Q D E K S R L T L M T A T A Q P L
2835 GGGTGTGGCTCACTGAAGTCAGGTCAACTTGAGGTGGTTTGGATCGCGCGTTTAAAGTCAGGACGACAAACGGGGGGTGGGTCAAGGTGTGAAGATTAATTTACCAAT
945 G V A S L K S G Q L E V L D R L M O D D N R G V G Q G V K D N L P T
2944 CTTGAGAGTTTCGTGATCATCTGGAAGATGGACCGCTATTCGACGGAAGAAAGCAAACTCGTACGGAAGCTCGGTCATGCTATGCTGATCATGATCATCAT
982 P E S F V I M L E R W T A I A K E S K S A K L A Y P S M A V Y Q S S
3053 GGGAAATGCTACACCAATACGTTCAATGTCGGTAAATGGGCGGTACATTTGAAAGAAAGATTACCGTCTGCTCCACAGCTTTTACCATCGGAGCTGACGCTGTTAAA
1018 W T T C G G A C C A A T T C A T T C T A A A G A T G C A G T T G C C C T A C C G A C A A T C G G T T G C T T C A C A C A G A G T T G G G C G G A A T G C T C T T G G A C G G G A A G T A A G T A T T C C A C
3162 C T T G C G A C A A T T C A T T C T A A A G A T G C A G T T G C C C T A C C G A C A A T C G G T T G C T T C A C A C A G A G T T G G G C G G A A T G C T C T T G G A C G G G A A G T A A G T A T T C C A C
1054 L R A I H S K D A V A P T D Q S A L L L H T V G R E C S L D A K Y F H
3271 C C A A G T G C C T C A T G C A C G C G T C G A G A A A T T G G C A T C A G A T C T C G A C G C T T T T A C T A A C T T G C G A T C G G G A A G A G C T C G C T G C T T A C A A C A C G C G C T C G T
1091 P T C L M H G V E K L A I T I S T L F T N S G M R K T S L S L Q H D G S
3380 T G C T G G A C A A C C A A G G C G G T A T A C A G T T C C C A A T G G A G A T A C A A G C T T A C A A A T A G T A C T G A C G T A A
1127 L L D N Q G G I T V S P M E I Q A Y K I V L T

FIG. 28

Drosophila mannosidase II (X77652)

1 ATGTTGCGCAATACGTGGGGGTTTCGTTTGGTAATTTGCTCCGGCTGCTCTGGTTTCTCCAGCCTGTACATAATCTCAATTTTGGCGCGCGCGGACGCCACCAGA
2 M L R I R R R F A A L V I C S G C L L Y F L S L Y I L N F A A T T Q
110 TAAAGCCCAACTATGAGAACATTGAGAACACGCTGATGAGCTGAGGAAATGCTTTGCAGGAGCAGCGGGAGGATGCGGAATCTCAGGGGGCACTTGGCCAAAACATC
371 I K P N Y E N I E N K L H E L E N G L Q E H G E E M R N L R R L A K T S
219 CAATCGGCAGCATCCAATAAGACTCTCACTTAAAGTGGCTGTCTCCCGAGGCGAGGCAATGCCAAGATGTGGTCCAAGACGTGCCCAATGTGGATGTACAGATGCTG
721 N R D D P I R P L K V A R S P R P G Q C O D V V Q D V P N V D V Q M L
328 GAGCTATACGATCCGATGCTCTCAAGGACATAGATGGAGGCGTGTGGAAACAGGGCTGGAACATTAACTACGATCCATGGAATGACAAACGCCCATCAACAAATAAAAG
1101 E L Y D R M S F K D I D G G V W K O G W N I K Y D P L K Y N A H H K L K
437 TCTTGCTTGTGGCCGACCTCGCACAACGATCTGGATGGATTACAGAGCTTGAAGAACTACCCAGCAGACCAACGACATCTCTGTCCAAGCTACTCGGCATCTGCA
1461 V F V P H S H N D P G W I Q T F E E Y Y Q H D T K H I L S N A L R H L M
546 CGACAATCCGAGATGAAGTTCATCTGGCGGGAATCTCTACTTGTCTGGTCTATACGATTGGGAGAGAAACAAAAGCTGCAGATGAAGTCCATTGTAAAGAAT
1821 D N P E M K F I W A E I S Y F A R F Y H D L G E N K K L Q M K S I V K N
655 GCAGACTTGAATTTGTGACTGGAGATGGGTAAATGCGCGGACAGGCCAATCTCCACTGGGCAAAAGCTATGCTGCAGCTGACCGAAGGGCAAACTGGTTGAAGCAAT
2191 G O L E F V T G W V M P D E C C T T G G A N S H W R N V L L Q L T E G O T W L K T
764 TCATGAATGTCACACCACTGCTCTGGGCACTCGATCCCTTGGACACAGTCCCACTATCCGTACATTTTGCAGAAAGTGGTTTCAAGAAATGCTTATCCAAAG
255 F M N V T P T A T S W A I O P F G H S P T M P Y I L O K S G F K N M L I O R
873 GAGCAGCTATTCCGTTAAGAACGAATGGCCCAACAGCGACAGCTTGACTTCTGTGGCGCCAGATCTGGGACAAACAAAGGGGACACAGCTCTCTCACCACATGATG
2911 T H Y S V K K E L A Q O R L E F L W R Q I W D N K G D T A L F T H M M
982 C C C T T A C T C G T A C G A C A T C C T C A C T G T G G T C C A G A T C C C A A G G T T G C T G C A G T T C G A T T C A A A C G A A T G G C C T C C T C G G T T G A G T T G C A T G G A A G G
3281 P F Y S Y D I P H T C G P D P K V C Q F O F K R M G S F L S C P W K
1091 TGCGCGCGGTACATAGTACATAAATGTGCGACAGCCTCAGATCTGCTGGTTGATCAGTGGAGAAGAAGGGCGAGCTGTATCGCACAAACGCTGCTGCTGATTC
364 V P P R T I S D N V A A R T D L V D Q W K K K A E L Y R T N V L L I P
1200 GTTGGGTGAGCACTTCCGCTTCAAGCAGAACACAGGTGGGATGTCGACGCGCTGAATCGAAAGGCTGTGGAACACTCAACAGCGAGGCCCATCTCAATGTCCAG
4001 L G D D F R F K N T E W D V Q R V N Y E R L F E H I N S Q A H F N V Q
1309 GCGCAGTTCGGCAGCTCAGGAATACTTTGATCGAGTGACAGGCGGAAGGGCGGACAAAGCCGAGTTTCCACGTAAAGCGGTGACTTTTACATACGCCGATC
4371 A O F G T L Q E Y F O A V H O A E R A G Q A E F P T L S O D F F T Y A D
1418 RATCGGATAACTTGGAGTGGCTACTACACTCCCGCCGCTATCATAAAGCGCATGGACCGCGCTCTGATGCACTATGTACGTGCAGCAGAAATGCTTTCCGCTGGCA
473 R S D N Y W S G Y T S R P Y H K R M D R V L M H Y V R A E M L S A W H
1527 CTCTCGGAGCGGATGGCCCGCATCAGGAACTCTGGAGCAGGCGCGGAGGAGCTGATTGTTCCAGCACACGAGCGGATATACTGGGACAGCAAAAGCGCATGTA
5091 S W D G M A R I E R L E Q A R R E L S L F Q H H D G I T Q T A K H V
1636 GTCTCGACTACGAGCAACGTCAGGAAAGCTTTAAAGCCTGTCAAAATGGTAATGCAACAGTCGGTCTACCGATTGCTGACAAAGGCTCCATCTACAGTCCGGACT
5461 V V D Y E Q R M Q E A L K A C O M V M Q Q S V Y R L L T K P S I Y S P D
1745 TCAGTTTCTCGTACTTTACGCTCGACGACTCCCGCTGGCCAGGATCTGGTGTGGAGGACAGTGCAGAACCCATAATATGGGCGAGGATATACGCGCTCCAGGATG
5821 F S F S Y F T L D S R W P G S G V E D S R T T I L G E D I L P S K H V
1854 GGTGATGCAACACCTTCCCGGAGGAGCGCTGGTGGACTTTATGTATCAGTCCGTTGTGAAGCGTTACCGACTTGGCAACAACTCCGGTGGAGGCTCAG
6181 V M H N T L P H W R E Q L V D F Y V S S P F V S V T D L A N N P V E A Q
1963 GTGTCCCGGTTGGAGCTGGCACCAGACACTCAAAAGACTATCCACCACAAGGCTCCACCACAAGTACCGCATCATCTTCAAGGCTCGGTCGCCCGCATG
6551 V S P V W S W H H D T L T K T I H P Q G S T K Y R I I F K A R V P P M
2072 GTCTGGGCGCACTAGCTTTAAACCATCTCCGATCCCAAGCCAGGACACCTCGTATGACATCGAATCTTCTGCTCGTAAAAACCCGAGCTCGTTACCTATGGCCCAATA
6911 G L A T Y V L T I S D S K P E H T S Y A S N L L R K N P T S L P L Q O Y
21811 TCGGAGGATGTGAAGTTTGGCGACTCTCAGAGATCTCATTCGGCGTTGTAACGAGCCACTTGGCCTTTCCGAGCAGGGGTCTCTTAAGTCCATTACGCTTACT
7271 P E D V K F G D P R E I S L R V G N O P T L A F S E Q G L L K S I Q L T
2290 CAGGATAGCCACATGTACCGGTGCACTCAAGTTCTCAAGTATGGCTTGCATCGCATGGCGATAGATCCGTTGCCATCTCTGTTCTGCCCAATGGACGAGCTTCG
7641 Q D S P H P V H F K L Y G V R S H G D R S G A Y L F L P N G P A S
2399 CAGTCAGACTTGGCCAGCAGTGGTCTGGTACTAAGGGCAAACTGGAGTCGTCGTGAGCGTGGGACTCCGAGCGTGGTGACCAACAGCATATGCGCGGTTGGTG
8001 P V E L G O P V L V T K G K L E S S V S V G L P S V V H Q T I M R G G A
2508 ACTGAGATTGCAATCTCGTGGATATAGGCTCACTGGACAACACGAGGATCGTATGCGCTGGAGAGCGATATCAGACAGCGGGGATCTCTACAGCGGATCTCAAT
8361 P E I R N L V D I G S L D N T E I V M R L E T H I D S G D I F Y T D L N
2617 GGATTGCAATTTATCAAGAGCGCGCGTGGACAAAATACCTTTGCAGGCGCAACTATTATCCCATACCTTTCTGGTATGTTTATGAGGATGCCAATACCGGACTCACTC
8731 G L O F I K R R R L D K L P L Q A N Y Y I P S G M F I E A N T I R L T
2726 TCTCAGCGGTCCAACGCTGGGTGGATCTCTTGGCTCGGCGGAGCTAGAGATTATGAAGATCGTCCGCTGGCCAGCGATGATGAACCGCGGCTGGGACAGGGTGT
9091 L T G Q P L G G S L A S G E L I M O D R R L A S D E R G L G O O V
2835 TTTGCAACAAAGCGGCTGCTCATATTATCGGCTGGTCTGGAGAAGGTTAAACACTGTGTCCGACGCTCAAGCTTATCATCTGCCCGGCTATTGACAAGTGGCCCA
9451 L D N K P V L H I Y R L V L E K V N H C V R P S K L H P A G Y L T S A A
2944 CACAAAGCATCGCAGTCACTGCTGGATCCACTGGACAAGTTTATATTGCTGAAATAGTGGATCGGGGACAGGGGCAATTTGGTGGCGATCACTCTTCCGCTCGTG
9821 H K A S O S L L D L D K F I F A E N E W I G A Q Q O F G D D H P S A R
3053 AGGATCTCGATGTCTCGGTGATGAGACGCTTAAACAAGACTCGGGCAAAACCCAGCGAGTAGGCTACGTTCTGCACCGCACTAATCTGATGCAATGGCGGACTCCAGA
10181 E D L D V S V M R R L T A C T S S A T Q R V G Y V L H R T A N L M Q C G T P E
3162 CGAGCATACACAGAGCTGGATGTGTGCCACTACTGCCGAATGTGGCGAGATCGAGCGCAGCGCTCACTTCTCTGCAGAAATTTGGAGCATTTGGAGCATGGCATGGTG
10541 E H T Q K L D V C H L L P N V A R C E R T T L T F L Q N L E H L D G M V
3271 CGCGCGGAAGTGTGCCCATGGAACCGCGCTTATGTGAGCAGTCACTCAAGCTGA
10911 A P E V C P M E T A A Y V S S H S S

FIG. 29

Human mannosidase II (U31520)

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1 ATGAAGTTAAGCCGCGAGTTACCGTGTTCGGCAGTCCGATCTTCTGTGGTGATTCTTCGCTCTACCTGATGCTGGACCGGGGTCACTTAGACTACCCAGGAACC
2 M K L S R Q F T V F G S A I F C V V I F S L Y L M L D R G H L D Y P R N
110 CCGCCGCGGAGGGCTCTTCCCTCAGGGCCAGCTCTCAATGTTGCAAGAAAAATAGACCATTTGGAGCGTTTGCTAGCTGAGATAATAGAGATCATCTCAAATATTAG
37 P R R E G S F P Q G Q L S M L Q E K I D H L E R L L A E N N E I I S N I R
219 AGACTCAGTCATCAATTGAGTGAGTCTGTGGAGGATGGTCCGAAAAGTTACAAAAGCAATTCAGCCAAGGTGCTGGCTCAGATCTTCTGCCCTCACAATTATCCCTC
73 D S V I N L S E S V E D G P K S S O S N F S Q G A G S H L L P S Q L S L
328 TCAGTTGACACTGCAGACTGTCTGTTGCTTACAAAAGTGAAGTACAAATTCAGATGTCGAGATGTTGGATGTTTACAGTCTAATTTCTTTGACAATCCAGATGGTG
110 S V D T A D C L F A S Q S G S H N S D V Q M L D V Y S L I S F D N P D G
437 GAGTTTGGGAAGCAAGGATTGACATTACTTATGAATCTAATGAATGGGACACTGAACCCCTTCAAGTCTTGTGGTGGCTCATTTCCCAATACGACCCAGGTGGTGAA
146 G V W K Q G F D I T Y E S N E W D T E P L Q V F V V P H S H N D P G W L K
546 GACTTTCAATGACTACTTTAGAGACAAGACTCAGTATATTTTAAATACATGGTCTTAAAGCTGAAAGAAGACTCACGGAGGAAGTTTATTTGGTCTGAGATCTTTAC
182 T F N D Y F R D K T Q Y I F N N M V L K L K E D S R R K F I W S E I S Y
655 CTTTCAAAGTGGTGGGATATTAGATATTGAGAAGAAGTCTGTTAAAGTTTAAATAGAAAATGGTCAAGTCTGAAATTTGACAGGTGGTGGGTTATGCTGATG
219 L S K W W D I I D I Q K K D A V K S L I E N G Q L E I V T G G W V M P D
764 AAGCTACTCCACATTTATTTGCCCTTAATTTGATCACTAATTTGAAGGACATCAGTGGCTGGAAAATATATAGGAGTGAACCTCGGTCCGGCTGGGCTATTGATCCCTT
255 E A T P H Y F A L I D O L I E G H Q W L E N N I G V K P R S G W A I D P F
873 TGGACACTCACCAACATGGCTTATCTTAAACCGTGGTGGACTTTCTCATGCTTATCCAGAGAGTTCATTATGCAAGTTAAAAACACTTTGCACTGCCATAAAACA
291 G H S P T M A Y L L N R A G L S H M L I O R V H Y A V K K H F A L H K T
982 TTGGAGTTTTTTGGAGACAGAATTGGGATCTGGGATCTGTCACAGATATTTTATGCCACATGATGCCCTTCTACAGCTATGACATCCCTCACACTTGTGGACCTGATC
328 L E F F W R Q N W D L G S V T D I L C H M M P F Y S Y D I P H T C G P D
1091 CTAAAAATGCTGCCAGTTTGAATTTAAACGTTCTTCTGGAGGAGATTTGGTTGTCCCTGGGGAGTCCCCCAGAAAACAAATACATCTGGAATGTCCAAAGCAGGGC
364 P K I C C Q F D F K R L P G G R F G G C P W G V P P E T I H P G N V Q S R A
1200 TCGGATGCTAGATAGTACCGAAGCAAGTCAAGCTTTTCCAGCAAAAGTCTTCTGGCTCCACTAGGAGATGATTTCCGCTACTGTGAATACACCGGAATGGAT
400 R M L L D Q Y R K S K L F R T K V L L A P L G D D F R Y C E Y T E W D
1309 TTACAGTTTAAAGATTATCAGCAGCTTTTGTATTATGAATTTCTCAGTCCAAGTTTAAAGTTAAAGATACAGTTTGGAACTTTATCAGATTTTTTGTATCGCTCGGATA
437 L Q F K N Y Q O L F D Y M N S Q S K F K V K I O F G T L S D F F D A L D
1418 AAGCAGATGAACTCAGAGACAGAAGGGCAATCGATGTTCCCTGTTTAAAGTGGAGATTTTTTCACTTATGCCGATCGAGATGATCTTACTGGATGGCTATTTTAC
473 K A D E T Q R D K G Q S M F P V L S G D F F T Y A O R D D H Y W S G Y F T
1527 ATCCAGACCCCTTTTACAAACGAATGGACAGAATCATGGAATCTCTTAAAGGCTGCTGAAATTTCTTACTATTTCCGCTGAGACAAGCTCACAAATACAGATAAAT
509 S R P F Y K R M D R I M E S H L R A A E I L Y F A L R Q A H K Y K I N
1636 AAATTTCTCTCATCATCTTTACACGGCACTGACAGAAGCCAGAGGAATTTGGGAGTGTTCCTCAACATCATGATGCTATCACAGGAAGTCCAAAGACTGGTGGTTG
546 K F L S S S L Y T A L T E A R R N L G L F Q H M D A I T G T A K D W V V
1745 TGGATTATGGTACAGACTTTTCTTCTGTTAATGGTTTGGAGAGAAATTTGGAATTTCTTCTTATTGGGAAGGCAAACTCACATACGACTTACTCT
582 V D Y G T R L F H S L M V L E K I I G N S A F L L I G K D K L T Y D S Y S
1854 TCTGATACCTTCTCGGAGATGGATTGAAACAAAAATCACAAGATCTCTGCCACAAAAATATAATAAGGCTGAGTGCCGACCAAGTACCTTCTGGTCTATAAT
618 P D T F L E M D L K Q K S Q D S L P O K N I I R L S A E P R Y L V V Y N
1963 CCTTTAGAACAGACCAATCTCGTTGCTCTCAGTCTATGTGAGTTCCCGAGAGTGCAAGTGTTCTCTGCTTCAGGAAAACCTTGGAAGTTCAAGTCAGCGCAGTTT
655 P L E Q D R I S L V S V F V S S P T V Q V P S A S G K P V Q V S A V
2072 GGGATACAGCAATACTATTTAGAAACAGCTATGAGATCTCTTTCCAGGACATATACCGCCATTGGGACTGAAAGTGTATAAGATTTTGAATCAGCAAGTTCAAA
691 W D T A N T I S E T A Y E I S F R A H I P P L G L K V Y K I L E S A S S N
2181 TTCACATTTAGCTGATTATGCTTGTATAAGATAAAGTAGAAGATAGCGGAATTTTACCATAAAGAAATATGATAAATACTGAAGAAGGTATAACACTAGAGAACTCC
727 S H L A D Y V L Y K N K V E D S G I F T I K N M I N T E E G I T L E N S
2290 TTTGTTTACTTCGGTTTATCAAACTGCACTTATGAAGCAATGATGACTAAAGAGATGGTAAACACCATGAAGTAAATGTGCAATTTTATGATGTTGGAACCAAA
764 F V L L R F D O T G L M Q Q M M T K E D G K H E V N V O F S W Y G T T
2399 TTTAAAGACAAAAAGTGGTGGCTTCTTCTTACCTGATGGTAAAGCCAGCTTATGTTTACACAACACCGCCCTTGTGAGAGTGACACATGGAAGGATTTATTC
800 I K R D K S G A Y L F L P D G N A K P Y V Y T T P P F V R V T H G R I Y S
2508 GGAAGTGACTTGTCTTTTGGACATCTTACTCATAGAGTCCGACTATACACATACAGGGAATAGAAGGACAGTCTGTGGAAGTTTCCAATATTGTGGACATCCGAAA
836 E V T C F F D H V T H R V R L Y H I Q G I E G Q S V E V S N I V D I R K
2617 GTATATAACCGTGAGATTGCAATGAAAATTTCTTCTGATATAAAAGCCAAAATAGATTTTATCTGACCTAAATGGGTACCAGATTCAACTACAATGACATGACCA
873 V Y N R E I A M K I S S D I K S Q N R F Y T D L N G Y O I Q P R M T L S
2726 AATTGCCCTTTCAGCAAAATGCTATCCCATGACCAAAATGGCTATATCCAGGATGCCAAACATCGTTTGACACTGCTCTGCTCAGTCATTAGGGGTTTCGAGTTT
909 K L P L O A N V Y P M T M A Y I O D A K H R L T L L S A Q S L Q V S B L
2835 GAATAGTGGTCAGATTGAAGTTATCATGGATCGAAGACTCATGCAAGATGATAACTGTGGCCCTTGAGCAAGGTATCCAGGATAACAAAGATTACAGCTAATCTATTTCGA
945 N S G Q I E V I M D R R L M Q D D N R G L E O G I Q D N K I T A N L F R
2944 ATACTACTAGAAAAAGAGTGTGTTAATACGGAACAGAAAAAGAGTGGTCAAGTTATCTTCTCTCTAGCCACATACTTCTTCTCTCATGAATCATCCAGTCA
982 I L L E K R S A V N T E E E K K S V S Y P S L L S H I T S S L M N H P V
3053 TTCCAAATGGCAAAATAGTTCTCTCACTACCTTGGAGTGCAGGTTGAATTTCTCCATTACAGTCATCTTTCCTTGTGACATTCTGTTTAAATTTGAGAACAAAT
1018 I P M A N K F S S P T L E L O G E F T C S P L Q S S L P C D I H L V N L R T I
3162 ACAGTCAAAGGTGGGCAATGGGCACTCCAATGAGGCAAGCTTGAATCTTCCACAGAAAAAGGTTGATTGTGCGTTCTCTAGCAAGGACAGGCGCTTTTGTCTACT
1054 Q S K V G N H S N E A A L L I L H R K G G F D C R F S S K G G C T F L F C S T
3271 ACTCAGGGAAGATATTGGTACAGAACTTTTAAACAACTTTATTGTCGAAGTCTCACACCTTCATCACTATCCTTGATGATTCACCTCCCGGCACTCAGAAATATAA
1091 T O G K I L V Q K L L N K F I V E S L T P S S L S L M H S P P G T Q N I
3380 GTGAGATCAACTTGGTCCAATGGAATCAGCAATCCGAATCCAGTTCAGGTGA
1127 S E I N L S P M E I S T F R I O L R

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FIG. 30

[illegible]

1 ATGAAGCTGAAAAAGCAGGTGACAGTGTGTGGGGTGCACCTCTTCTGTGTGGCAGTCTTCTCGCTACCTCATGCTGCACCGAGTGCAACACGATCCCACCCGACAC
2 M K L K K Q V T V C G A I F C V A V S L Y L M L D R V Q H D P T R M
110 AGAATGGTGGGAAGTCCCCGGAGCAAAATTCTGTGCTGCAGAACCCGATAGCAGCTGGAGCAGTTTGGAGGAGAACCATGAGATATCAGCCATTATCAAGGA
37 Q N G G N F P R S Q I S V L Q N R I E Q L E Q L L E E I S H I K D
219 CTCCTGCTGGAGCTGACAGCAACCGACAGAGGGCCGCCGCCCTACTACACGGTCAATGGCTCTGGGTGGTGGCCACGGGAGGCCGCCAGCTCTCTC
73 S V L E L T A N A E G P P A M L P Y T V N G S W V V P P E P R P S F F
328 TCCATCTCCCCGAGGACTGCGGATTTGCTTTGGGGGGCGGGGTGAGAAGCCAGAGCTCGAGATGCTCACTGTGCGGAGGAGCTGCCGTTTGACAACCTGGATGGTG
110 S I S P O D C Q F A L G G R G Q K P E L O M L T V S E E L P F D N V O G
437 GTGTGTGGAGGCAAGGCTTCGACATCTCTACGACCCGACAGCTGGGATGCTGAAGACTCGAGGTGTTTGTGGTGCCCACTCTCACAATGACCCAGGCTGGATCAA
146 G V W R Q G F D I S Y D P H W D A E D L Q V F V P H S H N D P G W I K
546 GACCTTTGACAAGTACTACACAGGACGACCCAAACATCTCTAATAGCATGGTGTCTAAGCTGCAGGAGGACCCCGGGCGGCTCTCTCTGGGCAGAGCTCTCTTC
182 T F D K Y Y T E Q T Q H I L N S M V S K L Q E D P R R R F L W A E V S F
655 TTCCGCAAGTGTGGGACAACATCAATGTCAAAGAGAGCGGCACTCGAAGGCTGGTGGGAAACGGGCACTGGAGATGGCAGAGGAGCTGGGTGATCCGACATG
219 F A K W W D N I N V O K R A A V R R L V G N G O L E I A T G G W V M P D
764 AGGCCAATTCCCCTACTTTGCATTGATTCAGCCAGCTCATCGAAGGACACCGTAGGCTGGAGAGAAATCTTGGTGAACCCCCCTCTGGCTGGGCACTGGACCCCT
255 E A N S H Y F A L I D Q L I E G H Q W L E R N L G A T P R S G W A V D P F
873 TGGATACAGCTCCACCATGCTTACTCTGCGCGGTGCCAACTCACCAGCATGCTGATTGAGAGAGTGCATATGCCATCAAGAAGCAGCTTGTGCCACCCACAG
291 G Y S S T M P Y L L R R A N L T S M L I Q R V H Y A I K K H F A A T H S
982 CTAGAGTTCATGTGGAGGACAGCATGGGACTCGGACTCCAGGACAGACATCTCTGTGTCATGATGCCCTTCTACAGCTATGACGTCCCCCATACCTGTGGCCAGATC
328 L E F M W R Q T W D S D S T D I F C H M M P F Y S Y D V P H T C G P D
1091 CCAAGATCTGCTGCCAATTGATTTCAAACGCTGCTGCTGGTGGGCGCATCAATGCCCTTGGAGGTGCCACCCCGGGGCTACACAGAGGCCAAGCTGGCAGAGAGGGC
364 P K I C C Q F D F K R L P G G R I N C P W P P R A I T E A N V A E R A
1200 AGCCCTGCTTCTGGACCAATACCGGAAGTCCGACGCTGTTCCGAAGCAACGCTCTCTGGTGGCTCTGGAGATGACTCCGATATGACAAGCCCGGAGGATGGGAT
400 A L L L D Q Y R K K S Q L F R S N V L V L P L G D D F R Y D K P O E W D
1309 GCCCAGTTCCTCAACTACCAAGGCTCTTGACTTCTCAAGCAGGCGCTCACTCCATGTGCAGGCCAGTGTGGCACTTCTCTGACTATTTGATGCCCTGTACA
437 A Q F F N Y O R L F D F F N S R P N L H V O A Q F G T L S D Y F D A L Y
1418 AGAGGACAGGGGTGGAGCGCAGGGGGCGGCTCCAGGGTTTCTGTGCTGAGCGGGATTTCTTCTCTATGCGGACCGGGAGGATCATTACTGGACAGGCTATTACAC
473 K R T G V E P G A R P P G F P V L S G D F F S Y A D R E D H Y W T G Y Y T
1527 TTCCCGGCTTCTACAAGAGCTTAGACCGAGTCTCGAAGCCCACTCGCGGGGGCGAGAGTTCTGTACAGCTGGCTGCGAGCTCAGCTCCGCGCTCTGGGTCTGGCT
509 S R P F F K Y K S L D R V L E A H L R G A E V L Y S L A A H A R R S G L A
1636 GCGCGGTACCCACTGTCTGATTTCACTCTCTGACGGAAGCTCGGCGACATTTGGGCTCTTCCAGCATCAGATGCCATCACTGGCAGCGGCCAAGAGGAGCTGTGGTG
546 G R Y P L S D F T L L T E A R R L T G L F O H H D A I T G T A K E A V Y
1745 TGGCATATGGGCTCAGGCTTCTGCGCTCTCTTGTCAACCTGAAGCAGGTTCATCATTATGACGCCCACTATCTGGTCTGGGGACAAGGAGCTTACCATTGTACCC
582 V D Y G V R L R S L V N L K O V I I H A A H Y L G L D K E T Y H F D P
1854 TAGGGCGGCTTCTCTCAAGTGGATGACACTCGTAAAGTACGACGCGCTCCAGAGGACCGGTCAGTCCAGTGGATCTCTCGCCAGGTTTGTGCTCTATTCAAC
618 E A P F L Q V D D T R L S H D A L P E R T V I Q L D S S P R F V L F N
1963 CCACTGGAACAGGAGCGATTACGATGGTGTCTGCTGGTCAACTCTCCCGGCTGGCTGTCTTCTCGGAGAGGGTGACGCCCTGGCGCTGACAGATCAGCGCACT
655 P L E Q E R F S M V S L V N S P R V R V L S E E G O P L A V O I S A H
2072 GGAGCTCTGCCACCGAGGGGCTCTGAGCTTACACAGGTGCTGTGCGCTGTCCGCTGCCAGCCTGGGCTGCTGCGAGCTACAGTGGGCTGGATGGCA
691 W S S A T E A V P D V Y Q V S V P R L P A L G L G V L Q L Q L G L D G H
2181 CCGCAGCTGCCCTCTCTGTGCGCATCTACTCGACGCGCGGAGCTGTGCTGCTCAGCAGGCAAGCGTTTCTCTCGGTGTACTGACTTGGCAGCAGGCACTTC
727 R T L P L S S V R I Y L H G R Q L S V S R H E A F L R V I D S G T S D F
2290 GCGCTCAGCAACCGCTACATGAGGCTGTGGTTCTCAGGCTTACTGGGCTCTCAAGAGCATCCGAAGGGTGGATGAGGAGCAGCAGCAGGAGCTGGACATGCAAGTCC
764 A L S N R Y M Q V W F S G L T G L L K S I R R V D E E H E Q Q V D M Q V
2399 TTGTCTATGGCAGCCGTAGCTCCAAAGACAAGAGTGGAGGCTACCTCTTCTGCGCGATGGCGAGGCTAGCCCTACGTCCCAAGGAGGCCCGGTGCTGGGTGCTACT
800 L V Y G T R T S K D K S G A Y L F L P D G E A S T P S R P P C V S L
2508 GAAGGCCCTTCTTCTCAGAGGTGGTGGCTACTATGAGCAGATCACCAGCGGCTCGGCTTTACAATCTGCCAGGGGTGGAGGGGCTGTCTGGCATATCATCCC
836 K A L S S O R W L R T M S T F T R R S G F T I C O G W R G C L W T Y M P
2617 TGGTGACATCCGGGACTACGTCAACAAGGAGTGGCCCTGCACATCCATACAGACATCGACAGTCCAGGCTGCAGGCCGACGGTGTGTAAGAAGCTCCCCCTCAAG
873 W W T S G T T S T R S W P C T S I O T S T A R V Q P R R Y L L K K L P L Q
2726 CCAACTCTACCCCATGCCAGTCTAGGCTATATCCAGGACGACAGAGCGCTCAGGCTGCACACTGCCAGGCCCTGGGTGTCTAGCCTCAAAGATGGCCAGCT
909 A N F Y P M P V M A Y I Q D A Q K R L T L H T A Q A L G V S L K D G Q L
2835 GGAGGTGATCTGGACCGGCGGCTGATCGAGGATGACAACCGGGGCTAGGCCAAGGCTCAAGGACAACAGAACCTGCAACCTCTTCCGCTCTCTGCTAGAGCGG
945 E V I L D R R L M Q D D N R G L G G Q G L K D N K R T C N R F R L L E R
2944 CGAACCGTGGGCACTGAGGTCCAAGATAGCCACTTACAGCTACCCATCCCTCTCAGCCAGCTGACCTCCATGACTCTGAACGCGCCCGGCGCTGCTCTGCTCTAG
982 R T V G S E V Q D S H S T S Y P S L L S H L T S M Y L N A P A L A L P V
3053 CAGGATGAGCTCCAGGCGCTGGTCTGGCTCATTTATCTCTGGCTTCTCACTGCGCTGTGACTTCCACTGCTCAACCTACGTACGCTCCAGGCTGAGGAGGA
1018 A R M Q L P G P G L R S F M P L A S S L P C D F H L L N L R L Q A E E D
3162 CACCTTACCTCTCGGCGGAGACGCACTCATCTTACACCGCAAGGGTTTGTCTGCGGCTGGAGGCGCAAGAATTTGGGCTTCAACTGCACCACAAGCCAAAGCAAGTA
1054 T L P S A E T T G A T G T G G T A T T C C T C A G C C A A C T C T T G A C T T A C C T C T G G C T C C C G C C A A C G A G C A T G A C T T A T T G G
3271 GCGCTGGCGAGCCTTTCCATGGCTGGATGTGGTATTCTTCAGCCAACTCTTGACGTTACTGTACCTCTGGGCTCCCCGCTCCACAGCAGTACGACGTCTATTGG
1091 A L G S L F H G L D V V F L O P T S L Y P L A S P S N S T D G T V Y L
3380 AGCCCATGGAGATTGCTACCTTTCGCTCCGCTGGGTAG
1127 E P M E I A T F R L R L G

Insect cell mannosidase III (AF005034)

[illegible]

FIG. 34

Human lysosomal mannosidase II (NM_000528)

[illegible]

FIG. 35

Human cytoplasmic mannosidase II (NM_006715)

1 ATGGCGGCAGCGCCGCTTCTGAAGCACTGGCGACCACCTTTTACGGGGTGGAGAAGTTCGTGTCCCCGATCTACTTACCAGCTGTAACCTCCGCGGCAGGCTTTTGG
3 M A A A A F L K H W R T T F E R V E K F V S P I Y F T D C C N L R G R L F
110 GGGCGAGCTGCCCTGTGGCTGTGCTCTCCAGCTTCTGACGCGGGAGAGACTTCCCTACCAGGAGGAGCTCAGCGGGAGCTTCCGCGCGGCGAGCTCGGCGCAGCTT
37 G A S C P V A V L S S F L T P E R L P Y Q E A V O R D F R P A Q V G G D S F
219 CGGACCCACATGGCTGGACCTGCTGGTTCCGGGTGGAGCTGACCATCCGAGGACATGGGTGGCGCAGGAAGTTCACCTTTGCTGGGAAAGTGATGGAGAAGGCTCGGTG
73 G P T W T W T C W F R V E L T I P E A W V G G E V H L C W E S D G E G L V
328 TGGCGTGATGGAGAAGCTGTCCAGGTTTAAACAAAGAGGGGTGAGAAGACCACTATGCTCTGACTGACAGGCTGGGGGAAAGAGACCCCCGAAGGCTCAGCTCTCTATG
110 W R D G E P V Q G L T K E G E K T S Y V L T O R L G E R D P R S L T L Y
437 TGGAAAGTAGCTGCAATGGGCTCTGGGGGGCGGGGAAGGAAGCATGATTGCAGCCCTGACCTGAGAAGATATTCAGCTGAGCGGGCTGAGCTAGCTGTGTTCGA
146 V E V A C A N G L L G A G K G S M I A A P D P E K I F Q L S R A E L A V F H
546 CCGGATGTCCACATGCTCTGTGGTGTGAGCTGTGCTGGGCAATAGCCAAGGCTCGGGGAAGGCAACACGCGAGCTTCCAGGCGCTGTACACAGGCAATCAG
182 R D V H M L L V D L E L L L G I A K G L G K D N Q R S F Q A L Y T A N Q
655 ATGGTGAACTGTGTGACCTGCCAGCCGAGACCTTCCGAGTGGCCAGGCGCTGGCTCAGGTTTCTGGCCAATGGGGGTGAAAGGCAACACCACTCATG
219 M V N V C D P A Q P E T F P V A Q A L A S R F F G O H G G E S Q H T I H
764 CACAGAGGCTGCCACATGATACAGCTGGCTTTGGCCCTTCAAAGAGACTGTGAGGAATGTGCCCGAGCTGGGTACCGCCCTGCAGCTCATGGAGCGGAACCC
255 A T G H C H I D T A W L V P F K E T V R K C A R S W V T A L Q L M E R N P
873 TGAGTTCATCTTTGGCTGCTCCAGGCGCAGCAGCTGGAAATGGGTGAAGAGCGGCTACCTGGCTGTACTCCCGGATCCAGGAGTTCGGTGGCGTGGGAGCTTTGTG
291 E F I F A C S Q A Q L E W K Y S R Y P G L Y S R I Q E F A C R G Q F V
982 CCTGTGGGGGCGACCTGGGTGGAAATGGATGGGAACCTGCCAGTGGAGAGCCATGGTGAGGCAAGTTTGGAGGGCCAGAACTCTTTCTGCAGGAGTTTGGGAAGA
328 P V G G T W E M D G N L P S G E A M V R Q F L O G N F L Q E F G K
1091 TGGTCTGTGAGTTTGGCTGGCGGACACTTTTGGCTACTCAGCAGAGCTCCCCAGATCATGCAAGGCTTGGCATCAGGCGCTTTCTCACCAGAAATTGAGCTGGAA
364 M C S E F W L P D T F G Y S A Q L P Q I M H G C G I R R F L T O K L S W N
1200 TTTGGTGAACCTTTCCCAACCATACATTTTCTGGAGGGCTGGATGGCTCCGCTGTACTTGGTCACTTCCCATGGGACTCTATGGGATCGAGGCGAGCGTG
400 L V N S F P H M D T F W E G L D G S R V L V H F P P G D S Y G M Q G S V
1309 GAGGAGGTGCTGAAGACCTGGCCAAACACCGGGACAAGGGCGGGGCCAACCAACAGTGCCTTCTCTTGGCTTTGGGAGTGGGGTGGTGGCCGCCACCCAGACATGC
437 E E V L K T V A N N R D K G R A N H S A F L F G F G D G G G O O P T Q T M
1418 TGGACCGCTGAAGCGCTGAGCAATACGGATGGGTGGCCAGGCTGGAGTCTTCTTCCAAAGACAGCTTCTCAGCAGTGGAGAGTGACTCAGAGCAGCTGTGCAC
473 L D R L K R L S N T D G L P R V O L T S S P R Q L F S A L E S D E Q L C T
1527 GTGGTTGGGGAGCTTCTTGGAGCTGCACATGGCAATACCCACCCATGCCAGATCAAGAAGGGGAACCGGGAATGTGAGCGGATCTGCACAGCAGCTGGAGCTG
509 V W G E L F L H N G T Y T T H A Q I K K G N R E C E R I L H D V E L
1636 CTGACTAGCCTGGCCCTGGCCCGCAGTGGCCAGTTCCTATACCCAGCAGCCAGCTGCAGCAGCTCTGGAGGCTCCTTCTTCTGAACAGTTCATGATGTGGTGACTG
546 L S S L A L A S A O F L Y P A A Q L Q H L W R L L L N H D V F H
1745 GAAGTGCATCAGATGGTGGCAGAGGAAGCATGTGCCATTATGAAGACATCCGTTCCCATGGCAATACACTGCTCAGCGCTGCAGCGCAGGCGCTGTGCTGGGGA
582 G S C I Q M V A E E A M C H Y E D I R S H G N T L L S A A A A A L C A G E
1854 GCGAGGCTCTGAGGCGCTCTCATGCTCAACACATGCCCTGGAAGCGGATGGAAGTATGGCTGCCCAAACCGGGCGGGCCAGAGCTAGCCCTGGTGCAGCTG
618 P G P E G L L I V N T L P W K R I E V M A L P K P G G A G S L A L V T V
1963 CCGCAGCTGGGCTATGCTCTGTCTCTCCCCCAGCTCAGTGCAGCGCTGTGCTGCCCGAGCGCTGTGCTGAGTGCAGAGACTGATGGCTCGTCACTTGGCA
655 P S M G Y A P V P P P T S L Q P L L P Q Q P V F V V Q E T D G S V T L D
2072 ATGGCATCTCCAGTGAAGCTGGACCCAACTGGTGGCTGAGCTCTTGGTCTGTGGTGGCTTGGCAGGAGGCGCATGCTCAGGCGCGCTGGGGAACCACTTTG
691 N G T A T T G A T G A T C C C C T T G A T C G G A T G C A T G G G A C T C A T G G A C T A C C A C T G G A C A C G G A A G C T G T G C T G G G C A G G C A G G A C C T G G C A C T G G G A C C
2181 G C T A T T T G A T G A T C C C C T T G A T C G G A T G C A T G G G A C T C A T G G A C T A C C A C T G G A C A C G G A A G C T G T G C T G G G C A G G C A G G A C C T G G C A C T G G G A C C
727 L F D V P L Y W D A W D V M D Y H L E T R K P V L G O A G T L A V G T
2290 GAGGCGCGGCTCGGGGCGAGCGCTGGTTCTTGTCTACAGATAGCGCCAAAGAGTGGGCTTAGCGAGGAGTTGTGCTGGACGTTGGCTGCCCTATGTGCGCTTCCACA
764 E G G L R G S A W F L L Q I S P N S R L S Q E V L D V G C P Y V R F H
2399 CCGAGGTACCTGGCATGAGGCGCCAAAGTCTCTGAAGGTGGAGTTCCTGCTCGGCTGGGAGTTCGCGGCGCACTATGAGATCAGTTTGGGCACTTGCAGCGCTGCAGCGAC
800 T E V H W H E A H K F L K V E F P A R V R S S O A T Y E I Q F G H L Q R P
2508 T A C C C A C T A C A A T A C C T T T G G G A C T G G G C T G A T T T G A G G T G T G G G C C A T C G T G G A T G A T C T G C A G A A C C G G T T T G G G T G G C C T G C T C A A G C A C T G C A A G
836 T H Y N T S W D W A R F E V W A H R W M D L S E H G F G L A L L N D C K
2617 T A T G G C G C T C A G T G C G A G G C A C A T C T C A G C T C T C G C T T T G C G G G C G C C T A A A G C C C G G A C G C A C T G C T G C A C A G G G C C C A C G A C T C A C C T A T G C A C T G A
873 Y G A S V R G S I L S L S L L R A P K A P D A T A D T G R H E F Y A L
2726 T G C C C A C A A G G G C T T T T C C A G G A T G T G C G G T T A C A A G T G C C T A C A G C T A A A C T C C C C T G T T G G C T T C C C A G G C C C C A G G C C C C C C C C C C A C T C T G T
509 M P H K G S F O D A G V I O A Y S L N F L L A L P A S R P A T S W
2835 G A G T G C G T T T T C G T G T C T C A C C C G C G G T C G T A T T G G A G A C C G T C A A G C A G G C G A G A G C A G C C C C A G C C G C G T C G T G G T C T G A G G C T G A T G A G G C A C G G C
945 S A F S V S S P A V V L E T V K Q A E S S P O R R S L V L R L Y E A H G
2944 A G C C A C T G G A C T G G T G G C T G C A C T T G C C T C C G G T T C A G G A G G C A C T C T C G C A T C T T G G A G C G A C A G A C C T G C T G G C C A C T T G A C T T C G G A C A A C C C G
582 S H V D C W L H L S L P V Q E A I L C D L L E R P D P A G H L T S G Q P
3053 C T A A G C T C A C C T T T T C C C T C C A A G T G C T G C C T G T G C T G C A C C T C C G C A C A C T A G T C C C T G G G G C T G G G G T T T G T G A A A G C C T G C G G G
1018 P E A H L F S L P S A V P V A R A S A S A T L S P W G W G F V C R R L C T G G G
3162 A C T C T A A T T C G C T C C C C A G C T A A
1054 L L I S A S P A

Figure 36A

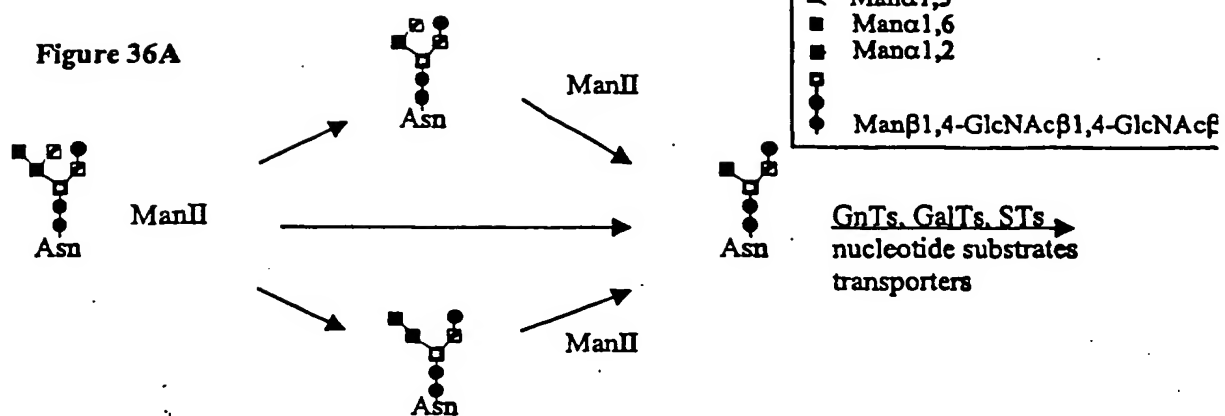


Figure 36B

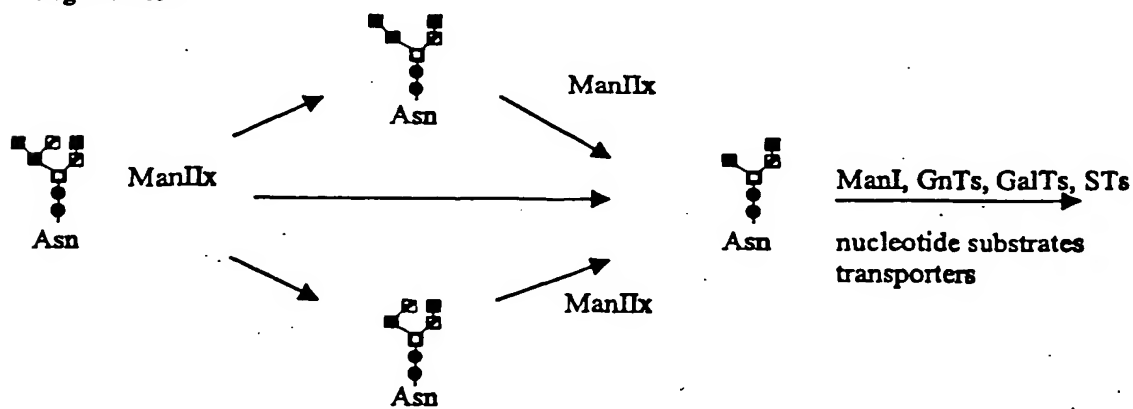


Figure 36C

